

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 28, 2005, 16:13:19 ; Search time 675 Seconds  
(without alignments)  
9190.947 Million cell updates/sec

Title: US-10-688-011-1

Perfect score: 1048  
Sequence: 1 attctgctctctgttagatga.....agtcacaataaaaaaaaaa 1048

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*  
1: geneseq1980s:\*  
2: geneseq1990s:\*  
3: geneseq2000s:\*  
4: geneseq2001as:\*  
5: geneseq2001bs:\*  
6: geneseq2002as:\*  
7: geneseq2002bs:\*  
8: geneseq2003as:\*  
9: geneseq2003bs:\*  
10: geneseq2003cs:\*  
11: geneseq2003ds:\*  
12: geneseq2004as:\*  
13: geneseq2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1048	100.0	1048	3	AAA12616	Aaa12616 cDNA enco
2	441	42.1	1050	2	AAQ71520	AaQ71520 Horset ph
3	426.2	40.7	1341	2	AAQ71523	AaQ71523 Yellowjac
4	49.2	4.7	460	8	ABX47675	Abx47675 Bovine ES
5	49	4.7	1301	4	ABL06057	AbL06057 Drosophila
6	49	4.7	4016	4	ABL06056	AbL06056 Drosophila
7	47.4	4.5	4590	5	AAH24065	Aah24065 Yeast AOD
8	47.2	4.5	1584	12	ADP28939	Adp28939 Human sec
9	47	4.5	3564	13	ADQ38815	Adq38815 Human sec
10	46.8	4.5	1526	6	ABL60540	AbL60540 Human l1p
11	46.8	4.5	3635	6	ACH03823	AbC03823 Human l1p
12	46.2	4.4	13326	6	ABL33713	AbL33713 Human imm
13	45.8	4.4	2000	8	ADA71938	Ada71938 Rice gene
14	45.8	4.4	7786	6	ABA92788	AbA92788 Buchnera
15	45.6	4.4	1383	10	AD123369	Ad123369 Mouse LpD
16	45.6	4.4	1605	6	ABK63642	AbK63642 Rat seque
17	45.6	4.4	1605	10	ADB82543	AdB82543 Primary r
18	45.6	4.4	1639	10	ADB57969	AdB57969 Toxicity-
19	45.6	4.4	2056	10	AD123667	Ad123667 Mouse LpD
20	45.2	4.3	1383	6	AAD27797	Aad27797 Human pan

21	45.2	4.3	1404	6	AB159436	Ab159436 Nucleotide
22	45.2	4.3	1422	6	ABN87363	Abn87363 Human l1p
23	45.2	4.3	1428	13	ADQ89959	Adq89959 Antagonis
24	45.2	4.3	1540	6	ABN60002	Abn60002 Novel hum
25	45.2	4.3	2352	4	AA03848	Aa03848 Human l1p
26	45.2	4.3	3549	2	AAV41319	Aav41319 Human l1p
27	45.2	4.3	3549	2	AAZ2183	Aaz2183 Human l1p
28	45.2	4.3	3549	2	ABE6907	AbE6907 Lung Canc
29	45.2	4.3	3549	6	ABT10903	Abt10903 Human bre
30	45.2	4.3	3549	6	ABT13006	Abt13006 Human l1p
31	45.2	4.3	3549	12	ADM41259	Adm41259 Human l1p
32	45.2	4.3	3549	13	ADR14098	Adr14098 Human NF-
33	45.2	4.3	3549	13	ADP23567	Adp23567 PRO polyP
34	45.2	4.3	3549	13	ADR73479	Adr73479 Human l1p
35	45.2	4.3	4075	10	ADB47407	AdB47407 Human CDN
36	45.2	4.3	4314	12	ADQ23742	Adq23742 Human 80F
37	45	4.3	3185	6	AA172633	Aa172633 Human 232
38	44.6	4.3	17294	6	AB132987	Ab132987 Human imm
39	44.4	4.2	421	8	ABX42958	Abx42958 Bovine ES
40	44.4	4.2	453	8	ABX36741	Abx36741 Bovine ES
41	44.4	4.2	938	5	AA07722	Aa07722 Human sec
42	44.4	4.2	1603	6	ABT13009	Abt13009 Human hep
43	44.2	4.2	1603	10	ADD29786	Add29786 Human tum
44	44.2	4.2	1767	2	AAx99572	Aax99572 Nucleic a
45	44.2	4.2	8634	6	AB133056	Ab133056 Human imm

## ALIGNMENTS

RESULT 1	AAA12616	standard; cDNA; 1048 BP.
ID	AAA12616	
XX	AAA12616	
AC	25-JUL-2000	(first entry)
XX		
DE	cDNA encoding a Pol a venom phospholipase A1 polypeptide.	
XX		
KW	Pol a venom; phospholipase A1; paper wasp; immune response; immunogen;	
KM	vespid venom; allergen-specific allergy; hymenoptera venom;	
KW	autoimmune condition; allergic condition; viral infection; HIV;	
XX	human immunodeficiency virus; Herpes Simplex virus; Papilloma virus; SS.	
OS	Polistes annularis.	
XX		
FT	Key	Location/Qualifiers
FT	CDS	1..963
FT		/*tag= a
FT	sig_peptide	/product= "venom phospholipase A1"
FT		1..54
FT		/*tag= b
FT	mat_peptide	55..963
FT		/*tag= c
XX		
PD	MO200018896-A1.	
XX	06-APR-2000.	
PF	01-OCT-1999;	99MO-US023211.
XX		
XX	01-OCT-1998;	98US-00166205.
XX		
PA	(UYRQ ) UNIV ROCKEFELLER.	
XX		
PI	King TP;	
XX		
DR	WFI; 2000-293139/25.	
DR	P-PSDB; AAY84613.	
XX		
PT	New nucleic acids encode enzymes of wasp venom, are useful to treat insect sting allergy or immune system-related disorders and differ from	

PT the genomic sequences in that introns have been removed.

XX PS Claim 5; Fig 1; 72pp; English.

XX CC The present sequence encodes a Pol a venom phospholipase A1 polypeptide, isolated from the paper wasp. The enzyme acts on phospholipid substrates, e.g. to hydrolyse fatty acids. The recombinant Polistamine venom is used to modulate an immune response to an immunogen in a mammal, particularly a vespid venom allergen-specific allergy, or allergy to other hymenoptera venom. Alternatively the venom enzyme is used to treat an immunologically affected disease or disorder, particularly a pathogenic disease or disorder, an autoimmune condition, an allergic condition, especially an allergy to hymenoptera venom, or a viral infection, especially human CC immunodeficiency virus (HIV), Herpes Simplex virus or papilloma virus. CC The enzyme is also useful to diagnose allergy

XX Sequence 1048 BP; 362 A; 160 C; 210 G; 316 T; 0 U; 0 Other;

Query Match 100.0%; Score 1048; DB 3; Length 1048;

Best Local Similarity 100.0%; Pred. No. 1.3e-232;

Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 ATTGCTTCTTGTAAATGATTCGACGACATTTAGAAATGTCCTTGAATAGAGCATG 60
DB 1 ATTGCTTCTTGTAAATGATTCGACGACATTTAGAAATGTCCTTGAATAGAGCATG 60
QY 61 TCTCCGATTTGATCTTTTATGAGAAAGATATAGTATTCATGTTTACTCAAGGATAG 120
DB 61 TCTCCGATTTGATCTTTTATGAGAAAGATATAGTATTCATGTTTACTCAAGGATAG 120
QY 121 CGAGATGTATTAATTTCTTAAGAAAGAACTTTAAGCAATTCAGATCTGTTTCAAAAGTCT 180
DB 121 CGAGATGTATTAATTTCTTAAGAAAGAACTTTAAGCAATTCAGATCTGTTTCAAAAGTCT 180
QY 181 ACAATATCAAAACAATTTGTTTCTTAATACATGTTTCTTCTTCACTGGGAATATGAA 240
DB 181 ACAATATCAAAACAATTTGTTTCTTAATACATGTTTCTTCTTCACTGGGAATATGAA 240
QY 241 AACTTGTCTATGTGCAAGCTTAAATAGAAAAGATGATTTCTTGTAAATTTGGGTC 300
DB 241 AACTTGTCTATGTGCAAGCTTAAATAGAAAAGATGATTTCTTGTAAATTTGGGTC 300
QY 301 GACTGGAAGAGGTCCTTGTAAATGCTTTTCTTCAACAAGAGATCTTTGGGTTATTC 360
DB 301 GACTGGAAGAGGTCCTTGTAAATGCTTTTCTTCAACAAGAGATCTTTGGGTTATTC 360
QY 361 AAAAGCGTTGGAACACACGTCACGTTGAAAAATTTGTGCTGATTTTCAAAACTACTT 420
DB 361 AAAAGCGTTGGAACACACGTCACGTTGAAAAATTTGTGCTGATTTTCAAAACTACTT 420
QY 421 GTAGAAAAATATTAAGTGTGATATCAATATATGATGAGGCACTGTTGGGCGCG 480
DB 421 GTAGAAAAATATTAAGTGTGATATCAATATATGATGAGGCACTGTTGGGCGCG 480
QY 481 CATACTTCAGGTTTTCGGGAAAAAGAGTTCAAAAGTTAAATTAGAAAAATACAAGAA 540
DB 481 CATACTTCAGGTTTTCGGGAAAAAGAGTTCAAAAGTTAAATTAGAAAAATACAAGAA 540
QY 541 ATTATCGGCTTGATCTGCTGACCGGTATTTTTCATCGAGAGTCTGTCGACACTT 600
DB 541 ATTATCGGCTTGATCTGCTGACCGGTATTTTTCATCGAGAGTCTGTCGACACTT 600
QY 601 TCGGTAAAGACGACGAGATATGTTCAAGTTATATACATCATCATATTAAGAGATAT 660
DB 601 TCGGTAAAGACGACGAGATATGTTCAAGTTATATACATCATCATATTAAGAGATAT 660
QY 661 TATATGTTGAGCGCTTGAATTTCTAAGTAAATATGAGAAAAATCACTGTTGCAT 720
DB 661 TATATGTTGAGCGCTTGAATTTCTAAGTAAATATGAGAAAAATCACTGTTGCAT 720
QY 721 GAACCATCTGCTCTCATACGAAAGCGTGAATATATCTAGTGAAGCTATAAAACATGA 780
DB 721 GAACCATCTGCTCTCATACGAAAGCGTGAATATATCTAGTGAAGCTATAAAACATGA 780

```

```

QY 781 TGTGTTTAAATGGAACACCATGAGAAATATTTCAGACCTCAAAAACCAATTTCCAG 840
DB 781 TGTGTTTAAATGGAACACCATGAGAAATATTTCAGACCTCAAAAACCAATTTCCAG 840
QY 841 TCGAGAGAGACACCTGTGTTTTCGTTGATGAAATGCAAAAAGTTATCTGCTAGAGC 900
DB 841 TCGAGAGAGACACCTGTGTTTTCGTTGATGAAATGCAAAAAGTTATCTGCTAGAGC 900
QY 901 GCATTTTATGACCGGTTGAAAGCAATGCACTTATTCGATTAAGAGGGAATTAACT 960
DB 901 GCATTTTATGACCGGTTGAAAGCAATGCACTTATTCGATTAAGAGGGAATTAACT 960
QY 961 TATATTAACCAAAAGTCAATGATACCAAAAATGATCATGATGATGATTAATGAAT 1020
DB 961 TATATTAACCAAAAGTCAATGATACCAAAAATGATCATGATGATGATTAATGAAT 1020
QY 1021 AAACGACAGTCAAAATTAATAAAAAA 1048
DB 1021 AAACGACAGTCAAAATTAATAAAAAA 1048

```

RESULT 2  
AAQ71520  
ID AAQ71520 standard; cDNA; 1050 BP.

XX AAQ71520;

XX AC 25-MAR-2003 (revised)

XX DT 26-APR-1995 (first entry)

XX DE Hornet phospholipase Dol mI, cDNA.

XX KW Hornet phospholipase; vespid venom enzyme; VV;  
allergen-specific allergic condition; Dol mI; ss.

XX OS Dolichovespula maculata.

XX FH Key Location/Qualifiers

XX FT CDS 1..951

XX FT /\*tag= a

XX PN W09420623-A1.

XX PD 15-SEP-1994.

XX PF 10-MAR-1994; 94WO-US002629.

XX PR 11-MAR-1993; 93US-00031400.

XX PR 11-JAN-1994; 94US-00180209.

XX PA (UNRO ) UNIV ROCKEFELLER.

XX PI King TP.

XX DR WPI: 1994-303030/37.

XX DR P-PSDB; AAR60599.

XX PT Nucleic acid encoding vespid venom enzymes - used to produce polypeptides for diagnosis and treatment of vespid venom allergen-specific allergic conditions.

XX PS Claim 7; Fig 1; 93pp; English.

XX AAQ71520 is the cDNA sequence that codes for hornet phospholipase (AAR60599), a vespid venom (VV) enzyme. These enzymes were used to produce highly specific and individualised polypeptides for the diagnosis and the treatment of VV-specific allergen specific conditions. For CC therapy, the polypeptides or fragments can be administered by oral, nasal or parenteral routes. (Updated on 25-MAR-2003 to correct PN field.)

XX SQ Sequence 1050 BP; 366 A; 170 C; 215 G; 299 T; 0 U; 0 Other;

Query Match 42.1%; Score 441; DB 2; Length 1050;  
 Best Local Similarity 67.0%; Pred. No. 3.7e-92;  
 Matches 665; Conservative 0; Mismatches 310; Indels 18; Gaps 2;

```

QY 65 CGGATGTTACTTTTAAATGAGAAAGATATGATCTTGTGTTACTCAAGGATAGCGAG 124
DB 56 CCGATGTCCTTTAGTAATGATACAGTAAAGATGATTTTAAACAAGGAAACCGAA 115
QY 125 ATGGTATTATTCTTAAGAAAGAACTTTAAAGAAATGATGATCTGTTTAAAGTCAAA 184
DB 116 AAGATGATTTTAACTGCTGATGATGAAACAGGCAATGATTAAGAGTCATCA 175
QY 185 TATCAAAAAGATGATTTCTTATACATGTTTCTTCAACCTGGGAATATCAAACT 244
DB 176 TAAAACTGCAATGATTAATCAATACGATGATTTTACCTGCTGCAACCGAAAAAAT 235
QY 245 TCGTGTATGTCGAAAGCTTTTAAATAGAAAAAGATGATTTCTGTAATTCGTCAGT 304
DB 236 TCGTGTATGTCGAGAGCTCTTATGCAATACAGTATTTCTTATTAATTAAGTCAAT 295
QY 305 GGAAGAAAGGCTGCTTGAATGCTTTTCTTCAACAAAGATGCTTGGTTATTCAAAG 364
DB 296 GGGGAGTGGCTGCTGTAATGATGATGATCCAGGCTGAAGTATATGTTTATTAAGGCTG 355
QY 365 CCGTGGAAACACACCTGACGTTGGAATTTGATGATTTTAAACAATCTACTGTAG 424
DB 356 CCGTGGTAAATACACGTTAGTGAATTTTACGCTATGATGCAAAAGAACTGTAG 415
QY 425 AAAATATAAAGTCTGATATCAAAATATACGATGATCGGGATGTTGGCGCGCAT 484
DB 416 AACATATTAAGTCCGATGACAAATATACGATCGTGGGACACAGTTTGGCGCACACA 475
QY 485 CTTCAGGTTTGGGGAAAAAGAGTTCAAAAGTTAAATTAAGAAAAATACAGAAATTA 544
DB 476 TTTCAGGTTTCGACAGGCAAAAGATTCAAGATTAATTAAGAAAAATTTCTGAATTA 535
QY 545 TCGGGCTGATCTGCTGACCGGATTTTTCATCGAATGATCTGCGGACAGCTTTGCG 604
DB 536 TTGGGCTGATCTGCTGAGGCTGATGTTCAAGAAAAATGTTTCCGAGAAATCTGCG 595
QY 605 TAAACAGCAGCAATATGTTCAAGTTATACATACATCAATATTAAGATATATATA 664
DB 596 AGACAGACGACATTAATGTAACAATTTTACATCATGACCAATTAAGAACAGAGAA 655
QY 665 ATGTTGATCGCTGATTTCTACGTGAATTAAGAAAAATCAACTGTTGC----- 717
DB 656 CTCTGGCACCGTCAATTTCTACATAAATACGAAATATCAACCGGTTGCAGATATA 715
QY 718 --AATGACATCTGCTCATACGAAAGCCGGAATATCTGATGATGATTAAC 775
DB 716 TTATGAGAACTGCTCATACGAGCCCGGAATATCTTACCGAGTGCATTAAGAC 775
QY 776 ATGATGTTGTTTAAATGAAACACATGAAAGAAATTTTACAGCATCTCAAAACCAATT 835
DB 776 GGGATGTTGTTTAAATGAGGCTCC-----GCAGTCAAGAAATCCGACCTGTT 826
QY 836 CCAAGTGCAGAGAGACCTGCTGTTGCGTTGATGAAATGCAAAAAAGTTATCTGCTTA 895
DB 827 CGAAGTGCACAAAGAAAGAGTGGCTTGGATTAACGCAAGAAATATCTTAA 886
QY 896 GAGGCGCATTTTATGACCGGTTGAAGCAAAATGCACTTATGCAATACAGAGGATTA 955
DB 887 GGGGCTCATTTTATGACCGGTTGAAGCTGAAGTCAATATGCAATTAACAGGGGAAA 946
QY 956 AACTTTAAATTAACAAAGTCAATGATACAAAAATGATCTATGATGATTAATAA 1015
DB 947 TAATTTAATTAATAAAAAAACAATTAATGACACAAAGTCAATTTGTAATGATGAAA 1006
QY 1016 TGAATTAACGAACGTCATTAATAAAAAA 1048
DB 1007 TGAATTAATTAACATTCAGAAAAA 1039

```

RESULT 3  
 AAQ71523  
 ID AAQ71523 standard; cDNA; 1341 BP.  
 XX  
 AC AAQ71523;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 26-APR-1995 (first entry)  
 XX  
 DE Yellowjacket phospholipase cDNA.  
 XX  
 KM Yellowjacket phospholipase; vespid venom enzyme; VV;  
 KM allergen-specific allergic condition; ss.  
 XX  
 OS Vesputia maculifrons.  
 OS  
 FH Key Location/Qualifiers  
 FT CDS 153..1052  
 FT /\*tag= a  
 XX  
 PN WO9420623-A1.  
 XX  
 PD 15-SEP-1994.  
 XX  
 PF 10-MAR-1994; 94MO-US002629.  
 XX  
 PR 11-MAR-1993; 93US-00031400.  
 PR 11-JAN-1994; 94US-00180209.  
 XX  
 PA (UYRQ ) UNIV ROCKEFELLER.  
 XX  
 PI King TP;  
 XX  
 DR WP1; 1994-303030/37.  
 DR P-PSDB; AAR60603.  
 XX  
 PT Nucleic acid encoding vespid venom enzymes - used to produce polypeptides  
 PT for diagnosis and treatment of vespid venom allergen-specific allergic  
 PT conditions.  
 XX  
 PS Claim 6; Fig 5; 93pp; English.  
 XX  
 CC AAQ71523 is the cDNA sequence that codes for yellowjacket phospholipase  
 CC (AAR60603), a vespid venom (VV) enzyme. These enzymes were used to  
 CC produce highly specific and individualised polypeptides for the diagnosis  
 CC and the treatment of VV-specific allergen specific conditions. For  
 CC therapy, the polypeptides or fragments can be administered by oral, nasal  
 CC or parenteral routes. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 1341 BP; 473 A; 206 C; 239 G; 423 T; 0 U; 0 Other;

Query Match 40.7%; Score 426.2; DB 2; Length 1341;  
 Best Local Similarity 66.9%; Pred. No. 1.1e-88;  
 Matches 660; Conservative 0; Mismatches 308; Indels 19; Gaps 3;

```

QY 64 CCGATTTGACTTTTAAATGAAAGATATGATTTCTATGTTTACTCAAGGATTAAGCA 123
DB 156 CCCAAATGCTCTTTTAAATCTGATACAGTTTCGATTAATTAAGAAACAGGAAAAACGA 215
QY 124 GATGATTAATCTTAAAGAAAGAACTTTAAAGCAATTAAGATGTTTCAAAAGTCTACA 183
DB 216 AATGATGATCTTAAATACACTACAGACATTAAGAAATCACTGAATTAAGAAAAAAGCT 275
QY 184 ATATCAAAAAGATGATTTCTTATACATGTTTCTTCAACCTGGAAATATGAAAC 243
DB 276 ATTAACAGTCCAGTTGATTTCAATTAACATGTTTCAATCTGCAAGTCAAAACAAAT 335
QY 244 TTGTTGCTATGTCGAAAGCTTTTAAATGAAAGATGATTTCTTGAATTTTGGTGCAG 303
DB 336 TTTCATTAATTTGCAAAAGCTTTGATGATTAAGATTAATGATGTTTCAATCGAT 395
QY 304 TGAAGAAAGGCTGTAATGCTTTGCTTCAACAAAGATGCTTTGGGTTATTCGAAA 363

```

```

Db      396 TGGCAGACGGCTGCTGTACTAATGAGCTGCAGTTTAAAGATTATATATCTACT 455
Qy      364 GCGTGGAAACACAGTACGTTGAGAAAATTGTAGCTGATTTTCAAAACACTGTGA 423
Db      456 GCGTGAAGAAATACAGTTTGTAGTGAATATATATGCTATGATCCGAAACCTGTA 515
Qy      424 GAAAAATATTAAGTGTGATATCAAAATATACATGATGCGGAGCTTTGGCGGCAT 483
Db      516 AAACACTATTAATATCGATATGCAAAATATACATTAATGATAGCTTAGAGACAT 575
Qy      484 ACTTCAGCTTTTGGGAAAAAGAGTTCAAAAGTTAAATTTAGAAAAATACAGAAAT 543
Db      576 GCTTCAGCTTTTGGCAGCAAAAAGCTTCAAGCTTAAATTTAGAAAAATATCTGAAT 635
Qy      544 ATCGGCTGATCTGCTGAGACCTGTATTTTATCATGAGAGCTGTCCGACGACTTGC 603
Db      636 ATTTGGCTGATCTCTGAGCCCTTGCTGATTAATCATATGTTCCGAAAGACTTGC 695
Qy      604 GTACACAGCAGCAATATGTTCAAGTTATATACATCATCATATATTAGAGATATAT 663
Db      696 GAGACAGATGCAAGATATGTTCAAAATATATACATCATCAACCTATTAGAACCGAAA 755
Qy      664 AATGTTGTAGCGTTGATTTCTACGTGAATATGAAAAAATCACTGCTGCAATGA 723
Db      756 ACCCTGTACCGCTCATTTCTACATGAATTAACGAAAGATCAACCTGCTGCTAGA 815
Qy      724 CCATCC-----TGCTCTCATAGAAACCGGAAATATCTGACGTAGTCATAAA 774
Db      816 TTTTCTCAGAACTTTGCTCTCATCTGAGAGCGGTATATACATGCTGAGTCATAAA 875
Qy      775 CATGAATGTTGTTTAAATTTGAAACACCATGGAAGAAATATTTGACACTCCAAAACCAAT 834
Db      876 CACGAATGTTGTTTAAATTTGGAATAC-----GAGTCAAAAGTTCCGACGCTATT 926
Qy      835 TCCCATGTCAGAGAGACACCTGTGTTTGGCTGATTTGAATGCAAAAAGTTATCTGCT 894
Db      927 TCGCTGTGACAAAGAGAGTCCGTTTGGTGAATTAACCCAAAGAGATATCTAGT 986
Qy      895 AGAGCGCATTTTATGACCGGTTGAAGCAAAATGACCTTATTTGCCATTAACGAGGAGTT 954
Db      987 AGAGGCTCATTTTATGATCCGTTGAAGATGCTTCTTTTTCATTAACAGGAGAG 1046
Qy      955 AAACCTTAATTAATAAACAAGTCAATGTAACAAAATGTATCTATGATGAATATTA 1014
Db      1047 ATATATTAATTAATAAATAAGT-AAATTCATTAATGCAAAATGATTTGTTAATGTGA 1105
Qy      1015 ATGAATTAACGAACGCTCAATTAATA 1041
Db      1106 ATGAATTAATTAACCATTTAACAATTA 1132

RESULT 4
ABX47675
ID      ABX47675 standard; cDNA, 460 BP.
AC      ABX47675;
XX      21-FEB-2003 (first entry)
DT      21-FEB-2003 (first entry)
XX      21-FEB-2003 (first entry)
DE      Bovine EST associated with lactation/muscle/fat deposition #12840.
XX      Bovine; ss; EST; expressed sequence tag; lactation; LMFD;
KM      muscle deposition; fat deposition; genome mapping; gene identification;
XX      gene analysis; cattle breeding.
OS      Bos Taurus.
XX      US2002137139-A1.
XX      26-SEP-2002.
XX      24-SEP-2001; 2001US-00960352.
XX

```

```

PR      12-JAN-1999; 99US-0115707P.
PR      11-JAN-2000; 2000US-00480902.
XX      (BYAT/) BYATT J C.
PA      (MATH/) MATHIALAGAN N.
PA      (TAON/) TAO N.
XX      (WARR/) WARREN W C.
PI      Byatt JC, Mathialagan N, Tao N, Warren WC.
XX      WPI; 2003-110599/10.
DR      New nucleic acid associated with lactation, and muscle and fat
PT      deposition, useful for genome mapping, gene identification and analysis,
PT      cattle breeding, or for genetically improving cattle.
XX      Claim 2; SEQ ID NO 12840; 245bp; English.
XX
CC      The invention relates to a purified nucleic acid molecule associated with
CC      lactation or muscle and fat deposition (designated LMFD), derived from
CC      cattle, and the LMFD nucleic acid can specifically hybridise to a second
CC      nucleic acid molecule comprising any of 15112 nucleotide sequences,
CC      appearing as ABX34836-ABX49947, or complements of them. Also included are
CC      ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic
CC      acid linked to a promoter and a 3' non-translated sequence that
CC      functions in the cell to cause termination of transcription and addition
CC      of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and
CC      (2) determining a level or pattern of a molecule in a bovine cell or
CC      tissue comprising: (a) incubating a marker nucleic acid (comprising any
CC      of the 15112 nucleic acid sequences or its complement or fragment) with a
CC      complementary nucleic acid molecule obtained from the bovine cell or
CC      tissue, where hybridisation between the marker nucleic acid and the
CC      complementary nucleic acid permits the detection of the molecule; and (b)
CC      detecting the level or pattern of the complementary nucleic acid, where
CC      the detection of the complementary nucleic acid is predictive of the
CC      level or pattern of the molecule. The LMFD nucleic acid is used for
CC      determining a level or pattern of a molecule in a bovine cell or tissue.
CC      It is useful for genome mapping, gene identification and analysis, cattle
CC      breeding, preparation of constructs for use in cattle gene expression, or
CC      for genetically improving cattle. The present sequence is one of the
CC      15112 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The
CC      present sequence was not shown in the specification but was obtained in
CC      electronic format from the USPRO web site:
CC      segdata.uspto.gov/sequence.html?docid=20020137139
XX
SQ      Sequence 460 BP; 116 A; 107 C; 129 G; 108 T; 0 U; 0 Other:
Query Match      4.7%; Score 49.2; DB 8; Length 460;
Best Local Similarity 51.4%; Pred. No. 0.14;
Matches 148; Conservative 0; Mismatches 128; Indels 12; Gaps 1;
Qy      359 CCAAGCCGTTGGAAACACAGCTACGTTGAGAAAATTGTAGCTGATTTTCAAAACATAC 418
Db      3 CCAAGCCGCGGGAATACCAAGCTGTGGAGACAGAGATGGCCAAAGTTTATGAATCGGA 62
Qy      419 TTGTAGAAAAATATTAAGTGTGATATCAAAATATATGATGATCGGCGATGTTGGCGG 478
Db      63 TGGCGGATGAATTTATACATATCCCTGGGCAATGTCATCTCTGGATATACGCTTGGGG 122
Qy      479 CGCATACTTCAGGTTTTCGGGAAAAAGAGTTCAAAAGTTAAATTTAGAAAAATACAGG 538
Db      123 CCCATGCTGCTGTGATTCAGGAAGTCTGACCAATTAAG-----AAGTCAACA 170
Qy      539 AAATTAATGGGCTGATCTCTGTGACCGTATTTTTCATCGAGATACGTCTCCGACACAG 598
Db      171 GATATACCGGCTTAATCACTGACCTTAACCTTGAATATGACAAAGCTCCAAAGTCCG 230
Qy      599 TTTGCGTAACAGACGCAATATGTTCAAGTTATACATACATCA 646
Db      231 TTTCTCTGATGATCGGATTTTGTAGAGCTTTTACACACATTCACA 278

```

RESULT 5



ID	AAH24065/c	standard; DNA; 4590 BP.
XX	AAH24065;	.
DT	29-AUG-2001	(first entry)
XX	DE	Yeast AOD9604-associated DNA sequence, SEQ ID NO:1.
XX	KM	Human growth hormone analogue peptide; hGH; AOD9604; lipid metabolism;
KW	lipogenesis inhibition; acetyl CoA carboxylase inhibition; obesity;	
KM	functional food; transgenic yeast; fat/lean ratio; food use; ds.	
XX	OS	Saccharomyces cerevisiae.
PH	Key	Location/Qualifiers
FT	misc_feature	10
FT	/tag= a	
FT	/note= "Represented as * in the specification"	
FT	3617	
FT	/tag= b	
FT	/note= "Represented as * in the specification"	
FT	3649	
FT	/tag= c	
FT	/note= "Represented as * in the specification"	
FT	3679	
FT	/tag= d	
FT	/note= "Represented as * in the specification"	
FT	3819	
FT	/tag= e	
FT	/note= "Represented as * in the specification"	
FT	3862	
FT	/tag= f	
FT	/note= "Represented as * in the specification"	
FT	3864	
FT	/tag= g	
FT	/note= "Represented as * in the specification"	
FT	3888	
FT	/tag= h	
FT	/note= "Represented as * in the specification"	
FT	3890	
FT	/tag= i	
FT	/note= "Represented as * in the specification"	
FT	3912	
FT	/tag= j	
FT	/note= "Represented as * in the specification"	
FT	3914	
FT	/tag= k	
FT	/note= "Represented as * in the specification"	
FT	3938	
FT	/tag= l	
FT	/note= "Represented as * in the specification"	
FT	3939	
FT	/tag= m	
FT	/note= "Represented as * in the specification"	
FT	3941	
FT	/tag= o	
FT	/note= "Represented as * in the specification"	
FT	3943	
FT	/tag= p	
FT	/note= "Represented as * in the specification"	
FT	4361	
FT	/tag= q	
FT	/note= "Represented as * in the specification"	
PN	WO200133977-A1.	
XX	17-MAY-2001.	

XX 06-NOV-2000; 2000MO-AU001362.  
PF  
XX  
PR 05-NOV-1999; 99AU-00003875.  
XX  
PA (META-) METABOLIC PHARM LTD.  
PI Belyea CI, Ng FM, Vaughan P;  
XX  
XX WPI: 2001-328876/34.  
DR  
XX  
XX New organisms containing nucleic acid encoding a growth hormone fragment  
PT which modulates lipid metabolism are useful to produce dietary aids for  
PR obesity and in the meat production industry.  
PS  
PS Disclosure; Page 48-50; 54pp; English.  
XX  
XX The invention relates to novel transgenic organisms useful in the  
CC production of functional food and drink products for the treatment or  
CC prevention of obesity via the regulation of lipid metabolism. The  
CC organisms comprise a polynucleotide encoding a growth hormone fragment  
CC capable of stimulating the activity of hormone-sensitive lipase (the key  
CC enzyme in lipolysis) and inhibiting acetyl CoA carboxylase (the key  
CC enzyme in lipogenesis). The growth hormone fragment preferably contains  
CC at least the disulphide-bonded loop of a mammalian growth hormone (but is  
CC not the full-length growth hormone) and is optionally linked to an  
CC epitope tag or heterologous fusion protein pattern. The transgenic  
CC organism may be a microorganism used to produce a fermented product  
CC (e.g., yeast), or an edible plant or animal or cell thereof. Food or  
CC drink made using methods of the invention are used to modify fat/lean  
CC ratio, lipid metabolism or food use in a mammal. In particular, the food  
CC or drink products may be used to treat or prevent obesity, particularly  
CC in humans, and may also be used to improve the fat/lean ration of  
CC livestock raised for meat production. In the exemplification of the  
CC invention, the human growth hormone (hGH) fragment analogue AOD9604 was  
CC expressed in yeast, optionally fused to the FLAG epitope (AAAT73625). The  
CC present sequence is described as a DNA sequence from yeast in the  
CC sequence listing, but is not further referred to in the specification  
SQ

Sequence 4590 BP; 661 A; 384 C; 127 G; 522 T; 0 U; 2896 Other;

Query Match 4.5%; Score 47.4; DB 5; Length 4590;  
Best Local Similarity 11.2%; Pred. No. 0.64;  
Matches 82; Conservative 319; Mismatches 329; Indels 0; Gaps 0;

92 TAGTATTCTTAGTTACTCAAGGGATGACGAGATGTATTATTCCTTAAGAAAAGAACTT 151  
::: |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
4466 HMRYYCNTKGNATYVANNAKATKNRTKKXSASCHSTNTKANHKANHGYSANKGANKG 4407  
  
152 TAACGAATTACGATCTGTTTACAAGAATCTCATATCAATAAACAAGTTGATTTCTTATAC 211  
::: |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
4406 HHVWASHHHVMASNMKFAKTNSMTGYVAUVSYUDSFRVANYAHNVHTCHADGM 4347  
  
212 ATGTTTCCTTTCAACTCGGGAATTAATAAACTTCGTTGATGTCGAAAGCCTTAATAG 271  
||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
4346 GTDATYCHSYHYHVASIGKSRHNWSGSHNHSRNNSSDSRRNWSRHNAHAGSSATKAS 4287  
  
272 AAAAAGATGATTTCTTGTAATTTCCGTCGACCTGGAAGAAGGTCCTTGAATGCTTTTG 331  
::: |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
4286 GHNYHWASSYVDHSVDDMVYGVTVKRANTKYMSKACKSSWMMSMMSMYHSTBTR 4227  
  
332 CTTCACAAAAGATGCTTTGGGTTATTCCAAAGCCGTTGANAACACGTCACGTTGGAA 391  
::: |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
4226 YBGVATATGSGSHNHSTBTSTRYBVATPKASGRHNWHSBTRSRVBGVATTKGSRHNWSTB 4167  
  
392 AATTGTAGCTGATTTTACAAAACACTACTTGTAGAAAAATATAAGTCTCATATCAATA 451  
::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
4166 TSRYBGVATATGASHNHWSBTRSYBVATPKASGRHNWHSBTRSRVBGVATTKGSRHNWG 4107  
  
452 TAGCATTTGATCGGCATAGTTTGGGCCGCGCATCTTCAGGTTTTGCGGAAAAAGAGTTC 511  
::: |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
4106 HMSHNNKDVSKSRHNWNMYHVVCARLYBEHVHNNRMWKCKKGKXGSYVKNNYVNCT 4047

Oy		512	AAATATTAAAAATTAGAGAAAATCAAGAAATTTATCGGGCTTGCCTGTCGACCGATT	571
Dd		4046	YUAYNHTTAANDYYCTYTATHTDMGNHTDDDKTKTYUTTTDHNKMDKGADKGDCKMCH	3987
Oy		572	TTCATCGGACTGTCTCCGACAGACTTGCGTGAACAAGCAGATAATGTTCAAGTTA	631
Dd		3966	DHDDNDGBBBBBBBBBBBBVKKSCNTTDCANDHDHNDGANDDNNDNDKKCYNRKR	3927
Oy		632	TACATCATCATCATATTTAGAGATATTTAATATGTTGTAAGCTGATTTCTACSTGA	691
Dd		3926	BHHHDHDBVYNNDNGMHNDHDHDDHNDHNMENDNVWBGHBVYWVYNNHHDDH	3867
Oy		632	ATTATGAGAAAAATACACTGCTGTCGAATGAACCATCTGCTGTATACGAAAGCGTGA	751
Dd		3866	VYNDNDGRDCANKKHMTGMGRKKHKAGHMSRHNKDSVKATKYCYKKKTCTCTTTY	3807
Oy		752	AATATCTAGCTGAGCGCATTAATAACATGAATGTTTATATGGAACACACATGAAGAAT	811
Dd		3806	ASTSNRYATMYTKHTATHTANATTAASNSWMGTDAYCSRNYPATATATADARVHAN	3747
Oy		812	ATTTCCAGCAC	821
Dd		3746	KBHITYASHNH	3737
RESULT 8				
ADP28939				
ID	ADP28939	standard; DNA; 1584 BP.		
XX				
AC	ADP28939;			
XX				
DT	12-AUG-2004	(first entry)		
XX				
DE	Human secreted protein encoding sequence SEQ ID #937.			
XX				
KM	Cytostatic; Antinflammatory; Immunosuppressive; Antibacterial; Virucide;			
KW	cancer; inflammatory; immune; ds; human secreted protein.			
XX				
OS	Homo sapiens.			
PN	WO2004035732-A2.			
PD				
XX	29-APR-2004.			
PF				
XX	28-AUG-2003; 2003WO-US026780.			
PR	29-AUG-2002; 2002US-0406576P.			
PR	29-AUG-2002; 2002US-0406579P.			
PR	29-AUG-2002; 2002US-0406585P.			
PR	29-AUG-2002; 2002US-0406588P.			
PR	29-AUG-2002; 2002US-0406608P.			
PR	29-AUG-2002; 2002US-0406611P.			
PR	29-AUG-2002; 2002US-0406612P.			
PR	29-AUG-2002; 2002US-0406616P.			
PR	29-AUG-2002; 2002US-0406642P.			
PR	29-AUG-2002; 2002US-0406646P.			
PR	29-AUG-2002; 2002US-0406653P.			
PR	29-AUG-2002; 2002US-0406655P.			
PR	29-AUG-2002; 2002US-0406666P.			
PR	17-SEP-2002; 2002US-0410946P.			
PR	17-SEP-2002; 2002US-0410947P.			
PR	17-SEP-2002; 2002US-0410948P.			
PR	17-SEP-2002; 2002US-0410949P.			
PR	17-SEP-2002; 2002US-0410951P.			
PR	17-SEP-2002; 2002US-0410951P.			
PR	17-SEP-2002; 2002US-0410956P.			
PR	17-SEP-2002; 2002US-0410959P.			
PR	17-SEP-2002; 2002US-0410960P.			
PR	17-SEP-2002; 2002US-0410961P.			
PR	17-SEP-2002; 2002US-0410962P.			
PR	17-SEP-2002; 2002US-0411019P.			
PR	17-SEP-2002; 2002US-0411022P.			

Query Match 4.5%; Score 47.2; DB 12; Length 1584;  
Best Local Similarity 45.9%; Pred. No. 0.55; Mismatches 238; Indels 12; Gaps 1  
Matches 212; Conservative 0;

CCGTTGAACAACAGCTCACGTTGAAAATTGTAGTATTTACAAACTACTTGTAAG 424

Db 371 CCGGGGGCTACACCAAACTGTTGGGACAGATGTGGCCCGGTTTATCACTGATGAGG 430  
 QY 425 AAAATATATAAGTGTGATATCAAAATATACATTTGATGGGCAATGTTGGCGGCA 484  
 Db 431 AGGAGTTTAACTACCTCTGACAAATGTCATCTCTTGGAAATACGCTTGAAGCCCATG 490  
 QY 485 CTTCAAGTTTTCGGGAAAAAGAGTTCAAAAGTTAAATTTAGAAAAATACAGAAATTA 544  
 Db 491 CTGGCTGGCATTCAGGAAGTCTGACCAATAG-----AAAGTCACAGATTA 538  
 QY 545 TCGGGCTTATCCTGTGACCGGTATTTTCATCGAGTACGTCCGACAGACTTGGC 604  
 Db 539 CTGGCTTCATCCAGCTGACCTTAATTGAGTATGACAAACCCCGATCTCTTCTTC 598  
 QY 605 TAACAGACGAGAAATGTTCAAGTATATCAATCAATCAATATATAGAGTATATTA 664  
 Db 599 CTGATGATGCAATTTTGTAGAGCTTTACACACATTCACGAGGGTCCCTGGTCA 658  
 QY 665 ATGTTGTAAGCGTTGATTTTCTACGTGAATATGAAAAATGAACTGTGTCATGAA 724  
 Db 659 GGATGGAATCCAGAAACAGTTGGGCAATGTTGACATTAACCGAATGAGGATCTTTC 718  
 QY 725 CATCTCTCTCATACAGAAAGCCGTGAATATCTGACTGATGATTAACATGAATTT 784  
 Db 719 AGCCAGGATGTAACTTGGAGAGGCTATCCGGTATTCAGAGAGAGACTTGGAGACA 778  
 QY 785 GTTATTTGGAACACCATGAGAAATATTTGAGCACTCCAA 826  
 Db 779 TCCCAATGAAACACTCTTGTGAATTTCTGCCGAGATACAA 820

RESULT 9  
 ADQ38815  
 ID ADQ38815 strand: DNA; 3564 BP.

XX AC ADQ38815;  
 XX DT 18-NOV-2004 (first entry)  
 DE Human SNP containing myocardial infarction-associated gene, SEQ ID 478.  
 XX KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;  
 XX KW cardiac; gene therapy; human; gene; ds.  
 XX OS Homo sapiens.  
 XX PN WO2004058052-A2.  
 XX PD 15-JUL-2004.  
 XX PF 22-DEC-2003; 2003WO-US040978.  
 XX PR 20-DEC-2002; 2002US-0434778P.  
 XX PR 10-MAR-2003; 2003US-0453135P.  
 XX PR 30-APR-2003; 2003US-0466412P.  
 XX PR 23-SEP-2003; 2003US-0504955P.  
 XX PA (APPL-) APPLERA CORP.  
 XX PI Cargill M, Devlin JI, Iakubova O;  
 XX DR WPI; 2004-533949/51.  
 XX DR P-PSDB; ADQ39643.  
 PT Identifying an individual who has an altered risk for developing  
 PT myocardial infarction by detecting a single nucleotide polymorphism in  
 PT the individual's nucleic acids.  
 XX PS Claim 7; SEQ ID NO 478; 145bp; English.  
 CC The invention relates to a novel method for identifying an individual who  
 CC has an altered risk for developing myocardial infarction. The method  
 CC comprises detecting a single nucleotide polymorphism (SNP) in any one of

CC the nucleotide sequences given in the specification in the individual's  
 CC nucleic acids, where the presence of the SNP is correlated with an  
 CC altered risk for myocardial infarction in the individual. The invention  
 CC further comprises: an isolated nucleic acid molecule comprising at least  
 CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in  
 CC the specification or its complement and encoding any one of the amino  
 CC acid sequences given in the specification; an isolated polypeptide  
 CC comprising an amino acid sequence given in the specification; an antibody  
 CC that specifically binds to the polypeptide or its antigen-binding  
 CC fragment; an amplified polynucleotide containing an SNP given in the  
 CC specification and which is between about 16 and 1000 nucleotides in  
 CC length; a kit for detecting an SNP in a nucleic acid, comprising the  
 CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a  
 CC nucleic acid molecule; a method of detecting a variant polypeptide; and a  
 CC method for identifying an agent useful in treating or preventing  
 CC myocardial infarction. The novel detection method has cardiac activity.  
 CC The nucleic acids of the invention may be used in gene therapy. The  
 CC method is useful in identifying an individual who has an increased or  
 CC decreased risk for developing myocardial infarction and for preparing a  
 CC composition for treating or preventing myocardial infarction. This  
 CC polynucleotide sequence represents a human myocardial infarction-  
 CC associated gene containing one or more SNPs of the invention. Note: This  
 CC sequence was not shown in the specification. The sequence has come from  
 CC an electronic sequence listing downloaded from the WIPO website.

SQ Sequence 3564 BP; 1021 A; 737 C; 802 G; 985 T; 0 U; 19 other;

Query Match 4.5%; Score 47; DB 13; Length 3564;  
 Best Local Similarity 50.7%; Pred. No. 0.74;  
 Matches 144; Conservative 1; Mismatches 127; Indels 12; Gaps 1;

QY 365 CCGTTGAAACACACAGTCAAGTGGAAATTTGTAGTATTTTCAAAACTACTTGTAG 424  
 Db 559 CCGGGGCTAACCAAACTGTGGACAGATGTCGCCGTTTATCAACTGATGAGG 618  
 QY 425 AAAATATATAAGTGTGATATCAAAATATACATTTGATGGGCAATGTTGGCGGCA 484  
 Db 619 AGGAGTTTAACTACCTCTGACAAATGTCATCTCTTGGAAATACGCTTGAAGCCCATG 678  
 QY 485 CTTCAAGTTTTCGGGAAAAAGAGTTCAAAAGTTAAATTTAGAAAAATACAGAAATTA 544  
 Db 679 CTGGCTGGCATTCAGGAAGTCTGACCAATAG-----AAAGTCACAGATTA 726  
 QY 545 TCGGGCTTATCCTGTGACCGGTATTTTCATCGAGTACGTCCGACAGACTTGGC 604  
 Db 727 CTGGCTTCATCCAGCTGACCTTAATTGAGTATGACAAACCCCGATCTCTTCTTC 786  
 QY 605 TAACAGACGAGAAATGTTCAAGTATATCAATCAATCAATATATAGAGTATATTA 664  
 Db 787 CTGATGATGCAATTTTGTAGAGCTTTACACACATTCACACAGA 830

# RESULT 10

ABL60540  
 ID ABL60540 strand: cDNA; 1526 BP.

XX AC ABL60540;  
 XX DT 27-AUG-2002 (first entry)  
 DE Human lipid metabolism enzyme (LME)-4 cDNA (clone Id: 7482937CB1).  
 XX KW Human; lipid metabolism enzyme; LME; cytosolic; neuroprotective; gene;  
 KW neurotropic; cerebroprotective; antiparkinsonian; antialzheimers; vaccine;  
 KW antisclerotic; antimicrobial; anti-AIDS; cardiovascular; antiangiinal;  
 XX KW gene therapy; protein therapy; ss.  
 XX OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT CDS 259..1365  
 FT /\*tag= a  
 FT /product= "lipid metabolism enzyme"



/note="LME-4"

W0200229036-A2.

11-APR-2002.

05-OCT-2001; 2001WO-US031302.

06-OCT-2000; 2000US-023838P.

13-OCT-2000; 2000US-024061P.

02-NOV-2000; 2000US-024571P.

08-NOV-2000; 2000US-0247503P.

17-NOV-2000; 2000US-0249503P.

(INCY-) INCYTE GENOMICS INC.

Harland L, Aryazu C, Das D, Griffin JA, Baughn MR, Ding L,

Malik NK, Yao MG, Lu Y, Elliott VS, Thangaveilu K, Ramkumar J,

Lal PG, Tribouley CM;

WPI; 2002-315862/35.

P-PSDB; ABB08004.

Lipid Metabolism Enzymes and nucleic acids, useful for preventing,

diagnosing and treating e.g. cancer, Alzheimer's disease and Creutzfeld-

Jakob disease.

Claim 5; Page 123; 127pp; English.

The invention relates to human lipid metabolism enzymes (LMEs) and

encoding polynucleotides. The LMEs can be expressed by standard

recombinant technology. The LME polypeptides, polynucleotides and

modulators may be used in the prevention, diagnosis and treatment of

diseases associated with inappropriate LME expression such as cancer

(e.g. myeloma, sarcoma and breast cancer), neurological disorders (e.g.

Parkinson's, Alzheimer's and multiple sclerosis), microbial infections

(e.g. Creutzfeld-Jakob disease and Acquired Immune deficiency syndrome

(AIDS)) and/or cardiovascular disorders (e.g. cardiomyopathy, angina

pectoris and mitral valve prolapse). The present sequence represents the

human LME-4 encoding cDNA

Sequence 1526 BP; 440 A; 303 C; 325 G; 458 T; 0 U; 0 Other;

Query Match

Best Local Similarity 4.5%; Score 46.8; DB 6; Length 1526;

Matches 160; Conservative 0; Mismatches 147; Indels 15; Gaps 1;

QY 318 TTGTAATGCTTTGCTTCAACAAGATGCTTGGGTTATTCACAAAGCGGTGGAACAC 377  
DB 312 TTGCAATTAATTTGATTTGATTCACAGGATACATCACTGCTTAACAATCT 371  
QY 378 ACCTCAAGTTGAAATTTGATCTGATTTTACAACTGTTGTAAGTAATTAAGT 437  
DB 372 CCGTGTGTTGGTGGAGGTGCTTATTTATTTGATGTTCTCATGAAAAATTTGAATA 431  
QY 438 GCTGATATCAATATACGATGATTCGGGCTATGTTGGCGGCTATCTTCAAGTTTGC 497  
DB 432 TTCCCTTTAAAGTACATGATGCTTGGCCACAGCTTGGAGCACACCTGCTGGGAGC 491  
QY 498 GGGAAAGAAGTTCAAAAGTTAAATTAAGAAATCAAGAAATTAATCGGGCTGATTC 557  
DB 492 TGG-----GTCAAGATACCAAGGCTTGAAGAAATTAATCGGGTGGAGCC 536  
QY 558 TGTGGAACGATATTTTATCGAGATGATCTGCGGACAGCTTGGCTTAACAGACGAGA 617  
DB 537 AGCTGGGCAATTTTCCACAACACTCAAGAAGATCAGGCTAGACCCCTGGATGCA 596  
QY 618 ATATGTTCAAGTTATACATCA 639  
DB 597 CTTGTTGAGCTTATTCATCA 618

RESULT 11

ACH03823  
ID ACH03823 standard; cDNA; 3635 BP.

ACH03823;

26-SEP-2003 (first entry)

Human cDNA differentially expressed in lung cancer #28.

Gene therapy; emphysema; ss; gene; chronic obstructive pulmonary disease;

respiratory disorder; lung cancer; asthma; human.

Homo sapiens.

US2003065157-A1.

03-APR-2003.

04-APR-2002; 2002US-00116802.

04-APR-2001; 2001US-0281593P.

(LASE/) LASEK A W.

Lasek AW;

WPI; 2003-540803/51.

New combination comprising cDNAs that are differentially expressed in

respiratory disorders, useful for diagnosing or treating respiratory

disorders e.g. lung cancer, chronic obstructive pulmonary disease,

emphysema or asthma.

Claim 1; Page; 39pp; English.

The invention relates to a combination comprising cDNAs or their

complements that are differentially expressed in respiratory disorder.

The combination is useful for preparing a composition for diagnosing or

treating respiratory disorders e.g. lung cancer, chronic obstructive

pulmonary disease, emphysema or asthma. The present sequence represents

human cDNA differentially expressed during lung cancer

Sequence 3635 BP; 1053 A; 752 C; 824 G; 1006 T; 0 U; 0 Other;

Query Match

Best Local Similarity 4.5%; Score 46.8; DB 9; Length 3635;

Matches 145; Conservative 0; Mismatches 127; Indels 12; Gaps 1;

QY 365 CCGTGGAAACACAGCTCACTGGAATTTGATCTGATTTTACAAACTACTGTAG 424  
DB 620 CCGGGGCTTACACCAAACTGTGGACAGATGTGCCCCGTTTATCACTGGATGAGG 679  
QY 425 AAAAATATTAAGTGTGATATCAATATATGATGATGCGGCTATGTTGGGCGCAT 484  
DB 680 AGGAATTTAATCACTCTGAGCAATGTCCATCTCTTGGATACAGCTTGAAGCCATG 739  
QY 485 CTTGAGTTTGGGGAAGAAAGTTCAAAAGTTAAATTAAGAAATTAAGAAATTA 544  
DB 740 CTGCTGGCATTCAGGAAGTCTGACCAATTAAG-----AAAGTCAAGAAATTA 787  
QY 545 TGGGCTTATCTCTGTGACCGTATTTTCAATCGAGATGATCTGCGGACAGCTTTGGG 604  
DB 788 CTGGCTTCATTCAGTGAACCTTAATTTGATGATGCAAGCCCGAGTCTGTTTTC 847  
QY 605 TAAACAGCAGAAATATTTCAAGTTATACATATCAATCATTA 648  
DB 848 CTGATATGCAATTTTGTGAGCTTTTACACATTCACACAGA 891

RESULT 12

ABL33713 standard; DNA; 13326 BP.

ABL33713

XX

AC ABL3713;  
 XX  
 DT 26-MAR-2002 (first entry)  
 XX  
 DE Human immune system associated gene SEQ ID NO: 1686.  
 XX  
 KW Human; immune system disease; cytosine methylation; antiasthmatic;  
 KW antiarteriosclerotic; antiasthmatic; cytosine methylation; antiasthmatic;  
 KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;  
 KW antineumatic; antineumatic; antidiabetic; antipsoriatic;  
 KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;  
 KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;  
 KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;  
 KW ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200200928-A2.  
 XX  
 PD 03-JAN-2002.  
 XX  
 PF 02-JUL-2001; 2001WO-EP007537.  
 XX  
 PR 30-JUN-2000; 2000DE-01032529.  
 XX  
 PR 01-SEP-2000; 2000DE-01043826.  
 XX  
 PA (EPIG-) EPIGENOMICS AG.  
 XX  
 PI Olek A, Piepenbrock C, Berlin K;  
 XX  
 DR WPI; 2002-130909/17.  
 XX  
 PT Nucleic acid comprising fragment of chemically modified gene, useful for  
 PT diagnosis and treatment of diseases associated with abnormal cytosine  
 PT methylation.  
 XX  
 PS Claim 1; SEQ ID NO 1686; 32pp + Sequence Listing; German.  
 XX  
 CC The present invention provides a number of human immune system associated  
 CC genes which are modified by the methylation of cytosines. The sequences  
 CC can be used in the diagnosis and treatment of immune system disorders,  
 CC including eye diseases such as retinopathy, neovascular glaucoma and  
 CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid  
 CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,  
 CC rheumatoid arthritis, psoriasis and inflammatory ulcerative bowel  
 CC diseases. The present sequence is a gene of the invention  
 CC  
 XX  
 SQ Sequence 13326 BP; 3846 A; 115 C; 2666 G; 6699 T; 0 U; 0 Other;  
 XX  
 Query Match 4.4%; Score 46.2; DB 6; Length 13326;  
 Best Local Similarity 46.7%; Pred. No. 1.5;  
 Matches 191; Conservative 0; Mismatches 208; Indels 10; Gaps 1;  
 XX  
 QY 66 GGAATCTACTTTAAGAGAAAGATTAATCTTCTTCTTCTCAAGGATTAAGGAGA 125  
 DB 12913 GGAATCTACTTTAAGAGAAAGATTAATCTTCTTCTTCTCAAGGATTAATG 12972  
 QY 126 TGGTATTATTTCTTAAGAGAAAGATTAATCAATTCATTCGTTTCAAGGATTAAT 185  
 DB 12973 TGGTATTATTTCTTAAGAGAAAGATTAATTCATTCGTTTCAAGGATTAAT 13032  
 QY 186 ATCAAAAGAGTTGATTTCTTAATACATGTTCTTCACTGGGATTAATGAAACTT 245  
 DB 13033 TATATTAATTTAATATGTTTAAATTTGTTATGTAAGAAATTAATTAATGAAT 13092  
 QY 246 CGTGTATATGCGAAGCTTTAATAGAAAGATTAATTTCTTGTATTTCCGTCGACTG 305  
 DB 13093 ATATGATATATATATATGAGATTTTGAAGAAATTAATTAATATATATATATAT 13152  
 QY 306 GAAGAAGGCTGCTGATATGCTTTGCTCAAGGATGCTTGGGTTATTCGAAGC 365  
 DB 13153 GAGAGATTTATTTAAGGAAATTTGATATATGTTATGAGAGCTTTGGTATTAATAT 13212

QY 366 CGTTGAAACACACGCTACGTTGAAA-----ATTGTAGCTGATTTTACAAAGC 415  
 DB 13213 TGATGGAGAACTGTGTGTTGAGATTTAAGAAAGATTTGATTTAAGTTAAAGCTA 13272  
 QY 416 TACTGTGAAAAAATTAAGTGTGATTAATCAATATACGATTATCGG 464  
 DB 13273 GTTGTGTGAAAAATTAAGAGAGTGAATGTTGATTAATTAAGTTAGAGG 13321  
 RESULT 13  
 ADA71938/c  
 ID ADA71938 standard; DNA; 2000 BP.  
 XX  
 AC ADA71938;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Rice gene, SEQ ID 5263.  
 XX  
 KW Plant; bacterial infection; fungal infection; viral infection; rice;  
 KW gene; ds.  
 XX  
 OS Oryza sativa.  
 XX  
 PN WO200300898-A1.  
 XX  
 PD 03-JAN-2003.  
 XX  
 PF 22-JUN-2001; 2001WO-IB001105.  
 XX  
 PR 22-JUN-2001; 2001WO-IB001105.  
 XX  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 XX  
 PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y,  
 PI Katagiri F, Qian S, Tao Y, Whitcham S, Xie Z, Zhu T, Zou G;  
 XX  
 DR WPI; 2003-175290/17.  
 XX  
 PT Identifying at least one gene involved in plant resistance or response to  
 PT pathogenic infection for conferring resistance or tolerance to a plant to  
 PT bacterial, fungal or viral infection by determining or detecting plant  
 PT gene expression.  
 XX  
 PS Claim 27; SEQ ID NO 5263; 899pp; English.  
 XX  
 CC The present invention relates to a method (M1) for identifying genes  
 CC involved in plant resistance or response to pathogenic infection. M1  
 CC comprises identifying a gene whose expression is significantly altered in  
 CC the incompatible interaction of plant gene expression relative to  
 CC expression of the gene in an uninfected plant, in a mutant plant that  
 CC does not express a gene associated with response to pathogenic infection,  
 CC or in a corresponding incompatible or compatible interaction. (M1) is  
 CC useful for conferring resistance to resistance or tolerance to a plant to  
 CC bacterial, fungal or viral infection. The present sequence was used to  
 CC illustrate the invention.  
 CC  
 XX  
 SQ Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;  
 XX  
 Query Match 4.4%; Score 45.8; DB 8; Length 2000;  
 Best Local Similarity 9.6%; Pred. No. 1.2;  
 Matches 72; Conservative 335; Mismatches 337; Indels 5; Gaps 2;  
 XX  
 QY 193 CAAGTGTATTTCTTAATACATGTTTCTTCACTGGGATTAATGAAGACTGCTGCT 252  
 DB 1016 TMTTAT 957  
 QY 253 ATGTGAAAGCTTTAATAGAAAGATTAATTTCTTGTATTTCCGTCGACTGGAAG 312  
 DB 956 YCGTGMMAAGRRMMAACWCCMMKMKMTSCMMKMKMTSCWYIMMGMARVAYYAM 897  
 QY 313 GGTGCTTAAATGCTTTTGTCTTCAAGAGATGCTTTGGGTTATTCGAAGCGCTTGA 372

```

Db      896 RRRRTTKMSRRRMYTMTKMTMTMTCMCAKMYATGATWMTMYTYTCYATCA 837
Qy      373 AACACAGTCACGTTGGAATAATTTAGTCAATTTTCAAAACTACTTTAGAAAAATAT 432
Db      836 KCKYKAMTKMTTAAACATATSRWRAMAGMKRKYOMRATYMRWRMCKKAGNAATMMK 777
Qy      433 ----AAAGTCTGATATCAAAATATACATGATGATGGGATAGTTGGCCGCACTTC 488
Db      776 SRYRWKMYKATRYMTWMMWMTWMSWRKMSYRMSGMRMRMSAWRYSRKKCACTKY 717
Qy      489 AGGTTTTCGGGAAAAAGATTCAAAATTAATTAATTAAGAAAATACAGAAATTAATCGG 548
Db      716 ASSARPTK-RAKSYRRRRMYKRWKMTYRIRYMSCRMTTRAMSRRRRMAGASMKSCW 658
Qy      549 GCTTATCTCTGTCGACCGTATTTTCATCGAGTCTCGGACAGACTTTGCGTAC 608
Db      657 MYRGARSMYSKYSKACCKKTRVMTSYMTGYMSYSKMSMTSKMSGMYGKMTTC 598
Qy      609 AGACGCAGAATATGTTCAATGATATACATCATCATATATAGAGTATATATATGT 668
Db      597 TMYTSMKSTRRSRKMGMSMSRMYRMWMMKMRKRKYMRKCTWRRCMCYRWGYTMY 538
Qy      669 TGGTAGCGTATTTTACGTGATTAATGAAAAAATCAACCTGTTCAATGAAACATC 728
Db      537 TTSRSRMYTGRYKARTSRKRMYMYRYKRYCMTYYTGMTKCSYMMRRTYCKAKKCCY 478
Qy      729 CTGCTCTCATACGAAACCGTGAATATCTGATGATGATTAACATGATGTTGTT 788
Db      477 AMCKKAAVSGMMWYWRKYSKMMRMSTKMMWMMYKCRSMKYGAKGCGCKMMYCSYG 418
Qy      789 AATGGAACACCATGGAAGAAATATTTGACACTCCAAAACCAATTTCCAGTCAGAG 848
Db      417 YMKWYTMYSKYKSRCKYMRMYKGMWMTMYSAVSMWMTYYYAKYMKYRKRGT 358
Qy      849 AGACACCTGTTGTTGCGTGAATGAATGCAAAAAGTATCCTGCTAGAGCGCATTTA 908
Db      357 MSYVGSYKRYCTTWCYMKCMRCYRRKMRKKTYSKRCYCMRYATCTWCCYRKRGW 298
Qy      909 TGCACCGTTGAAGCAATGACCTTAT 937
Db      297 YSRSMWRTAGKWKMSRMSRWCYSYSWK 269

RESULT 14
ABA92788
ID      ABA92788 standard; DNA; 7786 BP.
XX
AC      ABA92788;
XX
DT      27-MAR-2002 (first entry)
XX
DE      Buchnera sp. plasmid pLew DNA sequence SEQ ID NO:2.
XX
KM      Buchnera; cockroach-symbiotic bacterium; cockroach extermination;
      circular; db.
XX
OS      Buchnera sp.
XX
FH      Location/Qualifiers
FT      complement(346..1197)
FT      /tag= a
FT      /product= "repA1 protein"
FT      1514..2017
FT      /tag= b
FT      /product= "yghA protein"
FT      2357..2893
FT      /tag= c
FT      /product= "repA2 protein"
FT      3032..4591
FT      /tag= d
FT      /product= "LewA protein"
FT      4652..5743
FT      /tag= e
CDS

```

```

FT      /product= "LewB protein"
FT      5733..7160
FT      /tag= f
FT      /product= "LewC protein"
FT      7163..7786
FT      /tag= g
FT      /product= "LewD protein"
PN      JP2001292771-A.
XX
XX      23-OCT-2001.
XX
XX      07-APR-2000; 2000JP-00107160.
XX
XX      07-APR-2000; 2000JP-00107160.
XX
XX      (RIKA ) RIKAGAKU KENKUSHO.
XX
XX      WPI; 2002-126043/17.
XX
XX      A genomic DNA of cockroach-symbiotic bacterium.
XX
XX      Claim 5; Page 230-233; 237pp; Japanese.
XX
XX      The present invention describes a gene (I) derived from Buchnera sp.
XX      containing the DNA (a) or (b), (a) has a fully defined base pair sequence
XX      selected from a table of sequences found in the Buchnera sp. genomic DNA
XX      of ABA92787 given in the specification or is a DNA selected from
XX      complementary DNA sequences, and (b) is a DNA which hybridises with the
XX      DNA (a) and encodes a protein. Also described are: (1) a recombinant
XX      vector (II) containing (1); (2) a transformant (III) containing (II); (3)
XX      a genomic DNA of Buchnera sp. containing the sequence given in ABA92787;
XX      (4) a plasmid derived from Buchnera sp. containing DNA (c) or (d), (c) is
XX      a DNA containing a fully defined sequence given in ABA92788 or ABA92789
XX      and (d) is a plasmid which hybridises with a DNA; and (5) a method for
XX      the preparation of a protein in which (III) is cultured and the
XX      expression protein of the objective protein is collected from the
XX      resultant culture. The DNA is useful for developing agricultural
XX      chemicals for exterminating cockroaches. The present sequence represents
XX      the specifically claimed Buchnera sp. plasmid pLew, from the present
XX      invention.
XX
XX      Sequence 7786 BP; 2887 A; 867 C; 1213 G; 2819 T; 0 U; 0 Other;
XX
XX      Query Match      4.4%; Score 45.8; DB 6; Length 7786;
XX      Best Local Similarity 51.4%; Pred. No. 1.7;
XX      Matches 133; Conservative 0; Mismatches 122; Indels 4; Gaps 1;
XX
Qy      70 TGTACTTTTAAGAGAAAGATATAGTATCTATGTTTACTCAAGGATTAAGCAGATGCT 129
Db      1229 TTTTATATATATTTCAAAATATATAAAATTTTATTTTATCTTCAATATTAATTTT 1288
Qy      130 ATTATCTTAAGAAAGAACTTTAAGCATTCGATCGTTTACAAGCTCAATATCA 189
Db      1289 TTATATTTAAGAAATATATATCTTATTTTATTTTATATGAAATATATATTTATATA 1348
Qy      190 AAACAAGTGTATTTCTTATACA---TGATTCTTCAACTGGAGATATGAAAACTT 245
Db      1349 AAAATTAATATATTTTAAACATATGATTTTCAAGATTAACCTTAAACTT 1408
Qy      246 CGTTGCTATGTCGAAAGCTTTAATAGAAAAGATGATTTCTTGTAATTTGGTGCACG 305
Db      1409 AAAAGTTTATCTTAACTTTCTTAATTAATAAATAATATATTAATTAATTAATATAT 1468
Qy      306 GAAAGAGGAGCTGTGAAT 324
Db      1469 CAATAAATATTTTAT 1487

RESULT 15
AD123669
ID      AD123669 standard; cDNA; 1383 BP.
XX

```

AC ADI2369;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Mouse LPDL cDNA #2.  
 XX  
 XX lipase; LPDL; LPDLR; lipase deficiency; atherosclerosis;  
 KM fatty liver disease; dyslipidaemia; hypercholesterolaemia;  
 KM hypertriglyceridaemia; mixed dyslipidaemia; lipid deficient state;  
 KM lipoprotein deficient state; mouse; gene; ss.  
 XX  
 OS Mus sp.  
 XX  
 PN WO2003055995-A2.  
 XX  
 PD 10-JUL-2003.  
 XX  
 PF 23-DEC-2002; 2002WO-CM001998.  
 XX  
 PR 21-DEC-2001; 2001US-0341786P.  
 PR 10-JAN-2002; 2002US-0346603P.  
 XX  
 PA (WENX/) WEN X.  
 PA (STEM/) STEWART A. K.  
 PA (TSUI/) TSUI L.  
 PA (HEGE/) HEGELE R. A.  
 XX  
 PI Men X, Stewart AK, Tsui L, Hegeler RA;  
 XX  
 DR WPI; 2003-569444/53.  
 DR P-PSDB; ADI23670.  
 XX  
 PT Novel isolated LPDL or LPDLR lipase polypeptides, useful for identifying  
 PT substances that bind to the protein and which are useful for treating  
 PT diseases associated with lipase function e.g. atherosclerosis and  
 PT hypercholesterolemia.  
 XX  
 PS Claim 3; SEQ ID NO 5; 172pp; English.  
 XX  
 CC The invention relates to an isolated mammalian (e.g., human or mouse)  
 CC lipase polypeptide (polyp), e.g., LPDL (I) or LPDLR polyp (II). (I) or  
 CC (II) is useful for identifying substances which can bind with LPDL or  
 CC LPDLR polyp, and for identifying a compound that affects the binding of  
 CC LPDL or LPDLR polyp and an LPDL or LPDLR binding polyp. (I) or (II) or  
 CC their nucleic acid is useful for identifying a compound that affects LPDL  
 CC or LPDLR polyp activity or expression. (I) or (II) or their nucleic acid  
 CC is useful for detecting or monitoring a condition associated with  
 CC increased or decreased LPDL or LPDLR expression or activity in an animal,  
 CC where the condition is lipase deficiency, atherosclerosis, fatty liver  
 CC disease and dyslipidaemia, such as hypercholesterolemia,  
 CC hypertriglyceridaemia, mixed (combined) dyslipidaemia, lipid or lipoprotein  
 CC deficient states, and/or any other tissue or plasma disorders of lipid or  
 CC lipoprotein metabolism. The nucleic acid is useful for diagnosing the  
 CC presence of or a predisposition for a disorder in a subject which  
 CC involves detecting a germline alteration in the nucleic acid in the  
 CC subject. An inhibitor is useful for modulating triglyceride activity by  
 CC inhibiting expression or activity of (I) or (II). The nucleic acid is  
 CC useful as a probe or primer. The present sequence is used in the  
 CC exemplification of the invention.  
 XX  
 SQ Sequence 1383 BP; 423 A; 273 C; 277 G; 410 T; 0 U; 0 Other;  
 XX  
 Query Match 4.4%; Score 45.6; DB 10; Length 1383;  
 Best Local Similarity 51.9%; Pred. No. 1.3; Indels 15; Gaps 2;  
 Matches 161; Conservative 0; Mismatches 134; Indels 15; Gaps 2;  
 QY 448 AATATACGATTGATCGGCGATGTTGGCGCGCATCTTACGTTTTCGGGAAAGAA 507  
 DB 466 AATTTTCACCTTCATTGCGATGAGCTTAGGGGCTCATATTAGTGATTTAGAGAAAGATA 525  
 QY 508 GTTCAAAAGTTAAATAGAGAAATACAGAAATATCGGGCTTGATCTCTGAGACCG 567  
 DB 526 TTTCA-----TGGTCAACTTGGAGAAATTACAGAGTCTTGACCAAGCTGGACCA 573

QY 568 TATTTTCATCCGAGTGCATCTGCCGACAGACTTTGGGTAAAGAGCAATATGTTCA 627  
 DB 574 CAATTTTCTAGAAAGCCATCGAATGACGATTATATACAGAGTCAAAAGTTGAGAT 633  
 QY 628 GTTATACATACATCAATCATATA--TTAGAGATATATTAATGTTGGTAGCGTTGATTC 684  
 DB 634 GTCATCCACACATGATATCAAAAGTTGGGTATTTGAGAGCCATCGGGGACATTTGATTT 693  
 QY 685 TACGTGATTTATGAGAAAAATCAACCTGTTGCAATGAACCATCTCTCTCATACGAA 744  
 DB 694 TATCCAAATGAGAGAAACATCAGCCAGGTGTCTTACATCAATTTTTCAGAAACCAAT 753  
 QY 745 GCCGTGAAT 754  
 DB 754 TTTATTAAT 763

Search completed: April 28, 2005, 20:21:10  
 Job time : 684 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 28, 2005, 19:29:29 ; Search time 221 Seconds  
(without alignments)

7759.357 Million cell updates/sec

Title: US-10-688-011-1

Perfect score: 1048  
Sequence: 1 atttgccttctgttagatga.....agtcacataaaaaaaaaa 1048

Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA: \*  
1: /cgn2\_6/prodata/1/ina/5A COMB.seq: \*  
2: /cgn2\_6/prodata/1/ina/5B COMB.seq: \*  
3: /cgn2\_6/prodata/1/ina/5A COMB.seq: \*  
4: /cgn2\_6/prodata/1/ina/6B COMB.seq: \*  
5: /cgn2\_6/prodata/1/ina/PTUS COMB.seq: \*  
6: /cgn2\_6/prodata/1/ina/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1048	100.0	1048	3 US-09-166-205B-63	Sequence 63, Appl 1
2	1048	100.0	1048	4 US-09-806-658-1	Sequence 1, Appl 1
3	441	42.1	1050	1 US-08-180-209B-16	Sequence 16, Appl 1
4	441	42.1	1050	1 US-08-385-745-16	Sequence 16, Appl 1
5	441	42.1	1050	3 US-08-485-388-16	Sequence 16, Appl 1
6	441	42.1	1050	3 US-08-474-853-16	Sequence 16, Appl 1
7	441	42.1	1050	3 US-09-166-205B-16	Sequence 16, Appl 1
8	441	42.1	1050	5 PCT-US94-02629-16	Sequence 16, Appl 1
9	426.2	40.7	1341	1 US-08-180-209B-26	Sequence 26, Appl 1
10	426.2	40.7	1341	1 US-08-385-745-26	Sequence 26, Appl 1
11	426.2	40.7	1341	3 US-08-485-388-26	Sequence 26, Appl 1
12	426.2	40.7	1341	3 US-08-474-853-26	Sequence 26, Appl 1
13	426.2	40.7	1341	3 US-09-166-205B-26	Sequence 26, Appl 1
14	426.2	40.7	1341	5 PCT-US94-02629-26	Sequence 26, Appl 1
15	59	5.6	1141	4 US-09-806-708B-22	Sequence 22, Appl 1
16	47.8	4.6	5096	4 US-09-949-016-15105	Sequence 15105, A
17	46.4	4.4	1141	4 US-09-806-708B-22	Sequence 22, Appl 1
18	45.8	4.4	7786	4 US-09-790-988-2	Sequence 2, Appl 1
19	45.2	4.3	1401	4 US-09-411-132A-2	Sequence 2, Appl 1
20	45.2	4.3	2352	4 US-09-411-132A-1	Sequence 1, Appl 1
21	45.2	4.3	3549	4 US-09-054-372-39	Sequence 39, Appl 1
22	44.4	4.2	1603	4 US-09-949-016-35	Sequence 35, Appl 1
23	44.2	4.2	1767	4 US-09-601-198-72	Sequence 72, Appl 1
24	43.6	4.2	1493	1 US-08-340-820-24	Sequence 24, Appl 1
25	43.6	4.2	1493	1 US-08-593-535-24	Sequence 24, Appl 1
26	42.2	4.0	601	4 US-09-949-016-201237	Sequence 201237, A
27	42.2	4.0	601	4 US-09-949-016-201351	Sequence 201351, A

28	42.2	4.0	1168	4 US-09-270-767-662	Sequence 662, App
29	42.2	4.0	1168	4 US-09-270-767-15944	Sequence 15944, A
30	42.2	4.0	145241	4 US-09-949-016-17394	Sequence 17394, A
31	42.2	4.0	145241	4 US-09-949-016-17395	Sequence 17395, A
32	42	4.0	36159	3 US-09-749-588-3	Sequence 3, Appl 1
33	42	4.0	36159	4 US-10-135-687-3	Sequence 3, Appl 1
34	41.4	4.0	505	4 US-09-417-251A-3	Sequence 3, Appl 1
35	41.4	4.0	1659	4 US-09-949-016-4553	Sequence 4553, App
36	41	3.9	832	4 US-09-621-976-2813	Sequence 2813, App
37	40.8	3.9	72278	4 US-09-949-016-16113	Sequence 16113, A
38	40.6	3.9	1771	4 US-09-807-794A-158	Sequence 158, App
39	40.6	3.9	1771	4 US-09-866-028-36	Sequence 36, App
40	40.6	3.9	1771	4 US-09-905-125A-158	Sequence 158, App
41	40.6	3.9	1771	4 US-09-302-775A-158	Sequence 158, App
42	40.6	3.9	1771	4 US-09-906-700-158	Sequence 36, App
43	40.6	3.9	1771	4 US-09-944-457-36	Sequence 158, App
44	40.6	3.9	1771	4 US-09-903-603A-158	Sequence 158, App
45	40.6	3.9	1771	4 US-09-904-920A-158	Sequence 158, App

#### ALIGNMENTS

```
RESULT 1
US-09-166-205B-63
Sequence 63, Application US/09166205B
Patent No. 6372471
GENERAL INFORMATION:
APPLICANT: Te Piao KING
TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF VESPID VENOM ENZYMES,
FILE REFERENCE: 2313/0713805
CURRENT FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 70
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 63
LENGTH: 1048
TYPE: DNA
ORGANISM: Polistes annularis
US-09-166-205B-63

Query Match      100.0%; Score 1048; DB 3; Length 1048;
Best Local Similarity 100.0%; Pred. No. 3.9e-268;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATTTGCTTCTGTAGATGATTCGACGACATTAGAAATGTTACCTTGATAGAGCATG 60
DB 1 ATTTGCTTCTGTAGATGATTCGACGACATTAGAAATGTTACCTTGATAGAGCATG 60
61 TCTCCGATTGTACTTTTATATGAGAAAGATATGATTCTATGTTACTCAAGGATTAAG 120
QY 61 TCTCCGATTGTACTTTTATATGAGAAAGATATGATTCTATGTTACTCAAGGATTAAG 120
DB 61 TCTCCGATTGTACTTTTATATGAGAAAGATATGATTCTATGTTACTCAAGGATTAAG 120
121 CGAGATGTTATTTCTTTAAGAAAGAACTTTAAGCAATTAGCATCTGTTTACAAAGTCT 180
QY 121 CGAGATGTTATTTCTTTAAGAAAGAACTTTAAGCAATTAGCATCTGTTTACAAAGTCT 180
DB 121 CGAGATGTTATTTCTTTAAGAAAGAACTTTAAGCAATTAGCATCTGTTTACAAAGTCT 180
122 CGAGATGTTATTTCTTTAAGAAAGAACTTTAAGCAATTAGCATCTGTTTACAAAGTCT 180
QY 181 ACAATTCACAAACAGTTGATTTCTTATACATGTTTCTTCACTGGAGATATTAAGA 240
DB 181 ACAATTCACAAACAGTTGATTTCTTATACATGTTTCTTCACTGGAGATATTAAGA 240
181 ACAATTCACAAACAGTTGATTTCTTATACATGTTTCTTCACTGGAGATATTAAGA 240
QY 241 AACTTGTTGCTATGTCGAAAGCTTTAATAGAAAAGATATTTCTTGAATTTGGCTC 300
DB 241 AACTTGTTGCTATGTCGAAAGCTTTAATAGAAAAGATATTTCTTGAATTTGGCTC 300
241 AACTTGTTGCTATGTCGAAAGCTTTAATAGAAAAGATATTTCTTGAATTTGGCTC 300
QY 301 GACTGGAAGAGGCTCTTGTATGCTTTGCTTCAAGAGATCTTGGTTATTTTC 360
DB 301 GACTGGAAGAGGCTCTTGTATGCTTTGCTTCAAGAGATCTTGGTTATTTTC 360
301 GACTGGAAGAGGCTCTTGTATGCTTTGCTTCAAGAGATCTTGGTTATTTTC 360
QY 361 AAAGCGTTGGAACACACGTCACGTTGGAATTTGTGCTGATTTTCAAAACTACTT 420
DB 361 AAAGCGTTGGAACACACGTCACGTTGGAATTTGTGCTGATTTTCAAAACTACTT 420
```

```

Db      361 AAGCCGTTGSAACACACGCTCAGTTGAAAAATTTAGCTGATTTTACAAAACTACTT 420
Qy      421 GTAGAAAAATATTAAGTGTGATATCAATATATACATGATGCGGATGTTGGGCGG 480
Db      421 GTAGAAAAATATTAAGTGTGATATCAATATATACATGATGCGGATGTTGGGCGG 480
Qy      481 CATACTTCAGTTTTCGGGAAAGAGTTCAAAAGTTAAATTTAGAAAAATACAGAA 540
Db      481 CATACTTCAGTTTTCGGGAAAGAGTTCAAAAGTTAAATTTAGAAAAATACAGAA 540
Qy      541 ATTATCGGCGTTGATCTCTGCGAGCCGTATTTTCAATGAGAGTCTGTCCGACAGACTT 600
Db      541 ATTATCGGCGTTGATCTCTGCGAGCCGTATTTTCAATGAGAGTCTGTCCGACAGACTT 600
Qy      601 TGGTATACAGACGACAGATATGTTCAAGTTATATCATACATCAATCATATTTAGAGATAT 660
Db      601 TGGTATACAGACGACAGATATGTTCAAGTTATATCATACATCAATCATATTTAGAGATAT 660
Qy      661 TATATGTTGTAGCGTTGATTTCTACGTAAATTTATGAAAAAATCAACCTGGTGCAT 720
Db      661 TATATGTTGTAGCGTTGATTTCTACGTAAATTTATGAAAAAATCAACCTGGTGCAT 720
Qy      721 GAACCATCTGCTCTCATACAGAAAGCCGTGAATATCTGATGTCATTAACATGAA 780
Db      721 GAACCATCTGCTCTCATACAGAAAGCCGTGAATATCTGATGTCATTAACATGAA 780
Qy      781 TGTGTTTATTTGGAACACACATGAGAAATATTTGAGCATCTCCAAACCAATTTCCGAG 840
Db      781 TGTGTTTATTTGGAACACACATGAGAAATATTTGAGCATCTCCAAACCAATTTCCGAG 840
Qy      841 TCGAGAGAGACACCTGTGTGCTGTGATTTGATGATGCAAAAAAGTTATCTGTAGAGGC 900
Db      841 TCGAGAGAGACACCTGTGTGCTGTGATTTGATGATGCAAAAAAGTTATCTGTAGAGGC 900
Qy      901 GCATTTTATGACCGGTTGAGCAATGCACTTATTTGCCATACAGAGGATTAACCT 960
Db      901 GCATTTTATGACCGGTTGAGCAATGCACTTATTTGCCATACAGAGGATTAACCT 960
Qy      961 TATATTAACAAAGTCAATGATGACAAAAATGTATCTATGATGATTAATTAATGAAT 1020
Db      961 TATATTAACAAAGTCAATGATGACAAAAATGTATCTATGATGATTAATTAATGAAT 1020
Qy      1021 AAACGACAGTCAAATTAATAAAAAA 1048
Db      1021 AAACGACAGTCAAATTAATAAAAAA 1048

RESULT 2
US-09-806-658-1
; Sequence 1, Application US/0980658
; Patent No. 6652851
; GENERAL INFORMATION:
; APPLICANT: KING, Te Piao
; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF POLISTINAE VENOM ENZYMES, S
; FILE REFERENCE: 2313/1P138-US1
; CURRENT APPLICATION NUMBER: US/09/806,658
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 1048
; TYPE: DNA
; ORGANISM: Polistes annularis
US-09-806-658-1

Query Match      100.0%; Score 1048; DB 4; Length 1048;
Best Local Similarity 100.0%; Pred. No. 3.9e-268;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      61 TCTCCGATTTGACTTTTAAATGAGAAAGTATAGTATCTATGTTTACTCAAGGATAG 120
Db      61 TCTCCGATTTGACTTTTAAATGAGAAAGTATAGTATCTATGTTTACTCAAGGATAG 120
Qy      121 CGAGATGATATTTCTTAAGAAAGAACTTTAAGCAATTAAGATCTGTTTACAAAGTCT 180
Db      121 CGAGATGATATTTCTTAAGAAAGAACTTTAAGCAATTAAGATCTGTTTACAAAGTCT 180
Qy      181 ACAAATACAAAACAAGTTGATTTCTTTATACATGTTTCTTCACTGGGAAATATGAA 240
Db      181 ACAAATACAAAACAAGTTGATTTCTTTATACATGTTTCTTCACTGGGAAATATGAA 240
Qy      241 AACTCGTTGATGTCGAAAGCTTTAATAGAAAAAGATGATTTCTTGTAATTTCCGCTC 300
Db      241 AACTCGTTGATGTCGAAAGCTTTAATAGAAAAAGATGATTTCTTGTAATTTCCGCTC 300
Qy      301 GACTGAAAGAAAGGCTGTTGATATGCTTTTGCTTCAACAAAGATGCTTTGGGTTATTC 360
Db      301 GACTGAAAGAAAGGCTGTTGATATGCTTTTGCTTCAACAAAGATGCTTTGGGTTATTC 360
Qy      361 AAAGCCGTTGAAAAACACAGTCACGTTGAAAAATTTGATGCTGATTTTACAAACTACTT 420
Db      361 AAAGCCGTTGAAAAACACAGTCACGTTGAAAAATTTGATGCTGATTTTACAAACTACTT 420
Qy      421 GTAGAAAAATATTAAGTGTGATATCAATATATGAGATGATGCGGATGTTGGGCGG 480
Db      421 GTAGAAAAATATTAAGTGTGATATCAATATATGAGATGATGCGGATGTTGGGCGG 480
Qy      481 CATACTTCAGTTTTCGGGAAAGAGAGTTCAAAAGTTTAAATTTAGAAAAATACAGAA 540
Db      481 CATACTTCAGTTTTCGGGAAAGAGAGTTCAAAAGTTTAAATTTAGAAAAATACAGAA 540
Qy      541 ATTATCGGCGTTGATCTCTGAGACCGTATTTTCAATGGAATGATGTCGCCGACAGACTT 600
Db      541 ATTATCGGCGTTGATCTCTGAGACCGTATTTTCAATGGAATGATGTCGCCGACAGACTT 600
Qy      601 TCGTAAACAGACGCAATATGTTCAAGTTATACATACATCAATATTAAGATATAT 660
Db      601 TCGTAAACAGACGCAATATGTTCAAGTTATACATACATCAATATTAAGATATAT 660
Qy      661 TATATGTTGTAGCGTTGATTTCTACGTGAATTAAGAAAAAATCAACTGGTTGCAT 720
Db      661 TATATGTTGTAGCGTTGATTTCTACGTGAATTAAGAAAAAATCAACTGGTTGCAT 720
Qy      721 GAACCATCTGCTCTCATACAGAAAGCCGTGAATATCTGATGATGATTAATTAATGAA 780
Db      721 GAACCATCTGCTCTCATACAGAAAGCCGTGAATATCTGATGATGATTAATTAATGAA 780
Qy      781 TGTGTTTATTTGGAACACATGAGAAATATTTACAGACTCCCAAAACCAATTTCCGAG 840
Db      781 TGTGTTTATTTGGAACACATGAGAAATATTTACAGACTCCCAAAACCAATTTCCGAG 840
Qy      841 TCGAGAGAGACACCTGTGTGCTGTGATTTGATGATGCAAAAAAGTTATCTGTAGAGGC 900
Db      841 TCGAGAGAGACACCTGTGTGCTGTGATTTGATGATGCAAAAAAGTTATCTGTAGAGGC 900
Qy      901 GCATTTTATGACCGGTTGAGCAATGCACTTATTTGCCATACAGAGGATTAACCT 960
Db      901 GCATTTTATGACCGGTTGAGCAATGCACTTATTTGCCATACAGAGGATTAACCT 960
Qy      961 TATATTAACAAAGTCAATGATGACAAAAATGTATCTATGATGATTAATTAATGAAT 1020
Db      961 TATATTAACAAAGTCAATGATGACAAAAATGTATCTATGATGATTAATTAATGAAT 1020
Qy      1021 AAACGACAGTCAAATTAATAAAAAA 1048
Db      1021 AAACGACAGTCAAATTAATAAAAAA 1048

RESULT 3
US-08-180-209B-16
; Sequence 16, Application US/08180209B

```







NAME/KEY: CDS  
LOCATION: 1..951  
US-08-485-388-16

Query Match 42.1%; Score 441; DB 3; Length 1050;  
Best Local Similarity 67.0%; Pred. No. 4e-107;  
Matches 665; Conservative 0; Mismatches 310; Indels 18; Gaps 2;

QY 65 CGGATTGTACTTTTATGAGAAAGATATGATTTCTATGTTTACTCAAGGATAGCGAG 124  
DB 56 CCGATGTCCTCTTAGTAATGATACAGTAAAGATTTTAAACAGGAAACCGAA 115  
QY 125 ATGTATTATTTTAAGAAAGAACTTAAGATTGATTCGATTCGATTCAGAGCTACAA 164  
DB 116 AACATGATTTTATACCTAGATACAAAGACGACAAAGATTTAAGAAAGCAATCA 175  
QY 185 TATCAAAACAAGTTGATTTCTTATACATGATTTCTTCAACTGGGATATGAAACT 244  
DB 176 TAAAGCTCAGTTGATTCATTAACGATGTTTACTTGTCTGCAACGAAAGAAATTT 235  
QY 245 TCGTTGCTATGTGAAAGCTTTTATAGAAAAGATGATTTTCTTATATTCGTCGACT 304  
DB 236 TCGTTGCTATGTGAGAGCTTTATGATACAGTATGATTTTCTTATATTCGTCGACT 295  
QY 305 GGAAGAAGGCTGTTGATGCTTTTCTTCAAGAGATGCTTTGGGTTATTCGAAG 364  
DB 296 GGGGAGTGGCTGCTGTTGATGATGATACCGAGTCTGAAGTATATTTTATAGGCTG 355  
QY 365 CCGTTGGAACACACGTCACGTTGAAATTTGATGCTGATTTTCAAAACTACTGTAG 424  
DB 356 CCGTTGTTATACACGCTTAGTTGAAATTTTATCGTATGATCGCAAGAACTGTAG 415  
QY 425 AAAAATATAAGTCTGATATCAATATACGATGATGCGGACATGTTGGGCGCGATA 484  
DB 416 AACAAATATAAGTCCGATACAAATATACGATGATGCGGACACAGTTGGGCGCACACA 475  
QY 485 CTTCAGTTTGGGGGAAAAAGTTCAAAAGTTAAATATAGAAATATACAGGAATTA 544  
DB 476 TTTCAGTTTGGGAGGAGGAAAGTTCAAGATTAATTAAGAAATTTTCTGAATTA 535  
QY 545 TCGGCTTGAATCTGCTGACCGATTTTTCATCGAGTGACTGTCGAGACGATTTGCG 604  
DB 536 TTGGGCTTGAATCTGCTGAGGCTAGTTTCAAGAAATATGATTTGTCGAGAGATCTGCG 595  
QY 605 TAAACAGCGCAATATGTTCAAGTTATACATACATCAATATTAAGATATTTATA 664  
DB 596 AGACAGCGCAATATGTTCAAGTTTATACATACATCAATATTAAGATATTTAGAA 655  
QY 665 ATGTGTAGCGTTGATTTCTAGTGAATATGAAAGAAATCAACCTGTTGC----- 717  
DB 656 CTCTTGACACCGTGAATTTCTACATTAATATACGAGATTAATCAACCGTTGACATATA 715  
QY 718 --AATGACCATCTGCTCATACGAAACCGGAAATATGATGATGATGATTAAC 775  
DB 716 TTTATGGAAGAACTGCTCTCATACGAGACCGGAAATCTTTACGAGATGATTAAGAC 775  
QY 776 ATGATGTTGTTTATTTGAAACCATGAAAGAAATTTTACGACATCCAAACCAATTT 835  
DB 776 GCGAATGTTGTTTATTTGGGGTCCC-----GCAGTCCAAAGATCCGACGCTGTT 826  
QY 836 CCAGTGTGACAGAGACACCTGTGTTGCTGTTGATGATGCAAAAGTTATCTCGCTA 895  
DB 827 CGAAGTGCACAGAAAGAGAGTGGGTTGCTGATTTAAACGCAAGAAATATCTTAA 886  
QY 896 GAGGCGATTTTATGACCGGTTGAGCAATGCACTTATGTCATTAACGAGGAGTTA 955  
DB 887 GGGGCTCATTTTATGATCGGTTGAAGCTGAAGCTCATATTCGAATTAACAAGGAGAA 946  
QY 956 AACTTTATTTATTAACAAAGTCAATGATACAAAAATGATATCTATTGATGATTTAA 1015  
DB 947 TAAATTTATTTATTAACAAAGTCAATGATGATGATGATGATTTGTTAATGATGAA 1006  
QY 1016 TGAATTAAGACAGTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1048

Db 1007 TGAATTAATTCATTCATTCAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 1039

RESULT 6  
US-08-474-853-16  
Sequence 16 Application US/08474853  
Patent No. 6287559  
GENERAL INFORMATION:  
APPLICANT: King, Te-Piao  
TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF  
TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND  
TITLE OF INVENTION: HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED THEREON  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Klauder & Jackson  
STREET: 411 Hackensack Avenue  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,853  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/180,209  
FILING DATE: 11-JAN-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/031,400  
FILING DATE: 11-MAR-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 600-1-074 CIPB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201 487-5800  
TELEFAX: 201 343-1684  
TELEX: 133521  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1050 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..951  
US-08-474-853-16  
Query Match 42.1%; Score 441; DB 3; Length 1050;  
Best Local Similarity 67.0%; Pred. No. 4e-107;  
Matches 665; Conservative 0; Mismatches 310; Indels 18; Gaps 2;

QY 65 CGGATTGTACTTTTATGAGAAAGATATGATTTCTATGTTTACTCAAGGATAGCGAG 124  
DB 56 CCGATGTCCTCTTAGTAATGATACAGTAAAGATTTTAAACAGGAAACCGAA 115  
QY 125 ATGTATTATTTTAAGAAAGAACTTAAGATTGATTCGATTCGATTCAGAGCTACAA 184  
DB 116 AACATGATTTTATACCTAGATACAAAGACGACAAAGATTTAAGAAAGCAATCA 175  
QY 185 TATCAAAACAAGTTGATTTCTTATACATGATTTCTTCAACTGGGATATGAAACT 244  
DB 176 TAAAGCTCAGTTGATTCATTAACGATGTTTACTTGTCTGCAACGAAAGAAATTT 235  
QY 245 TCGTTGCTATGTGAAAGCTTTTATAGAAAAGATGATTTTCTTATATTCGTCGACT 304

```

|||||
236 TCGTGTCTATGTGAGAGGCTCTATGCAATACAGTGATTTCTTATTAATTAATGTCGANT 295
QY 305 GGAAGAAAGGTCGTTTGAATGCTTTTGCCTTCAACAAGAGATGCTTGGGTATTCGAAAG 364
Db 296 GGGGAGAGGTCGTTTGAATGCTTTTGCCTTCAACAAGAGATGCTTGGGTATTCGAAAG 355
QY 365 CCGTTGGAACACACGCTCAAGTGGAAAAATTTGAGCTGATTTTCAAAACTACTGTTAG 424
Db 356 CCGTTGATATACAGCTTATGGAATTTTATGCTATGATCGAAAGAACTTGTAG 415
QY 425 AAAATATATAAGTCTGATATCAATATACGATTGATCGGCAATGTTTGGCGCGCAT 484
Db 416 AACCAATATAAGTCGATGACAAATATACGATGCTGGGACACAGTTTGGCGCGCACAC 475
QY 485 CTTCAGTTTGGGGAAAAAGATTCAAAAGTTAAATTAAGAAATATACAGAAATTA 544
Db 476 TTTCAGGTTTCGAGGCAAAAGATTCAGAGATTAATAATTAAGAAATTTTCTGAATTA 535
QY 545 TCGGCTGTATCTGCTGACCGTATTTTCAATCGAGATGACTGTCGCAACAGCTTTGCG 604
Db 536 TTGGGCTTATCTGCTGAGCCCTAGTTTCAAGAAATATGATTTTCCGAGAGATCTGCG 595
QY 605 TAAACAGCAGAAATATGTTCAAGTTATACATACATCAATCATATTAGAGATATTATA 664
Db 596 AGACAGACGCACTATATGTAACAATTTTACATACATCGAGCAATTTAGAGACAGAGAA 655
QY 665 ATGTTGTAGCGTGTATCTGATTAATGAGAAATTAATCAACCTGTTGC----- 717
Db 656 CTCTTGGACCGTCGATTTCTACATATAATTAACGAAATATCAACCGGTTGCAATATA 715
QY 718 --AATGACCATCTGCTCTCATACGAAAGCCGTGAATATCTGATGATCATTAAC 775
Db 716 TTAATGGAAGAACTTCTCTCATACGAGAGCGGTGAATATCTTACCGAGTGCATAGAC 775
QY 776 ATGAATGTTGTTAATTGGAACCAATGAGAAATATTTCAAGACTCCAAACCAATTT 835
Db 776 GCGAATGTTGTTAATTGAGGATCC-----GCACTCAAGAAATCCGACGCTGTT 826
QY 836 CCAAGTCAGAGAGACACCTGTTGTTGAGATTTGAATGCAAAATTTATCCGCTA 895
Db 827 CGAAGTCAGAGAAACGAGTGGTGGTGGATTAACGAAAGAAATATCTTAAC 886
QY 896 GAGGCGCATTTTATGACCGGTTGAGCAATGACCTTATTTGCCATAAGAGGATTA 955
Db 887 GGGGCTCATTTTATGATGACCGGTTGAGGCTCAGATTTGCAATACAAAGGGAATA 946
QY 956 AACTTAAATTATTAACAAAGTCAATGTAACAAAAATGATCTATTGATGAAATTTAA 1015
Db 947 TAAATTAAATTATTAACAAAAATTAATTAATGACAAAGTCAATTTGTTAATGATGAA 1006
QY 1016 TGAATTAACGAACAGTCAATTAACAAATTAACAAATTAACAAATTAACAAATTA 1048
Db 1007 TGAATTAATTAACGATTCAGAAATTAACAAATTAACAAATTAACAAATTAAC 1039

```

```

RESULT 7
US-09-166-205B-16
; Sequence 16, Application US/09166205B
; Patent No. 6372471
; GENERAL INFORMATION:
; APPLICANT: Te Piao King
; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF VESPID VENOM ENZYMES,
; TITLE OF INVENTION: SUCH AS PHOSPHOLIPASE AND HYALURONIDASE, AND IMMUNOLOGICAL
; TITLE OF INVENTION: THERAPIES BASED THEREON
; FILE REFERENCE: 2313/013805
; CURRENT APPLICATION NUMBER: US/09/166,205B
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 1050
; TYPE: DNA

```

```

; ORGANISM: Dolichovespula maculata
US-09-166-205B-16
Query Match 42.1%; Score 441; DB 3; Length 1050;
Best Local Similarity 67.0%; Pred. No. 4e-107;
Matches 665; Conservative 0; Mismatches 310; Indels 18; Gaps 2;
QY 65 CCGATTGTAATTTTATGAGAAAGATATGATATCTATGTTTACTCAAGGGATTAAGCGAG 124
Db 56 CCGTATGTCCTTTAGTATATGATACAGTTAAGATATTTTAAACAGGAAACCGAA 115
QY 125 ATGTAATTAATCTTAAGAAAGAACTTTAAGCAATTAAGATCTGTTTCAAGTACAA 184
Db 116 AACATGATTTTATACGCTAGTATACATAGAACAGCAACATGAATTTAAGAAATCAATCA 175
QY 185 TATCAAAACAGTGTATTTCTTATACATGTTTCTTCAACTGGGAATATAGAAACT 244
Db 176 TAAACGTCAGATTTTATTAATTAACGATGTTTACTGCTGCAACCGAAAAATTT 235
QY 245 TCGTGTCTATGTGAAAGGCTTTAATTAAGAAAGATGATTTTCTGTAATTTGCTGACT 304
Db 236 TCGTGTCTATGTGAAAGGCTTTAATTAAGAAAGATGATTTTCTGTAATTTGCTGACT 295
QY 305 GGAAGAAAGGTCCTTGTATATGCTTTTGTCAACAAAGATGCTTTGGGTTATTCGAAAG 364
Db 296 GCGGATGAGCTGCTTGTATGATGATACCCAGTCTGAATATGTTTATTAAGGCTG 355
QY 365 CCGTTGGAACACACGTCACGTTGGAATTTGATGCTGATTTTCAAACTACTTTGAG 424
Db 356 CCGTTGGAATACAGCTTATGTTGAATTTTATGCTATGATGCAAAAGAACTTTGAG 415
QY 425 AAAATATATAAGTCTGATATCAATATATGATGATGAGGATGTTTGGCGCGCAT 484
Db 416 AACATATATAAGTCTGATATCAATATATGATGATGAGGATGTTTGGCGCGCACAC 475
QY 485 CTTCAGTTTGGGGAAAAAGATTCAAAAGTTAAATTAAGAAATTAACAGAAATTA 544
Db 476 TTTCAGGTTTCGAGGCAAAAGATTCAGAGATTAATAATTAAGAAATTTTCTGAATTA 535
QY 545 TCGGCTGTATCTGCTGACCGTATTTTCAATCGAGATGACTGTCGCAACAGCTTTGCG 604
Db 536 TTGGGCTTATCTGCTGAGCCCTAGTTTCAAGAAATTAATGATTTTCCAGAGAACTTGC 595
QY 605 TAAACAGCAGAAATATGTTCAAGTTATACATACATCAATCATATTAGAGATATTATA 664
Db 596 AGACAGACGCACTATATGTAACAATTTTACATACATGACGAAATTTAGAGAACAGAGAA 655
QY 665 ATGTTGTAGCGTGTATTTTACGTAATTAAGAAATTAATCAACCTGTTGC----- 717
Db 656 CTCTTGGACCGTCGATTTCTACATTAATAACGAAATTAACACCCGTTGCAATATA 715
QY 718 --AATGACCATCTGCTCTCATACGAAAGCCGTGAATATCTGATGATCATTAAC 775
Db 716 TTAATGGAAGAACTTCTCTCATACGAGAGCGGTGAATATCTTACGAGTGCATTAAC 775
QY 776 ATGAATGTTGTTAATTGGAACACCATGAGAAATATTTGACGACTCCAAACCAATTT 835
Db 776 GCGAATGTTGTTAATTGAGGATCC-----GCACTCAAGAAATCCGACGCTGTT 826
QY 836 CCAAGTCAGAGAGACACCTGTTGTTGAGATTTGAATGCAAAAGTTATCTGCTA 895
Db 827 CGAAGTCAGAGAAACGAGTGGTGGTGGATTAACGCAAAAGAAATATCTTAAC 886
QY 896 GAGGCGCATTTTATGACCGGTTGAGCAATGACCTTATTTGCCATAACGAGGATTA 955
Db 887 GGGGCTCATTTTATGATGACCGGTTGAGGCTCAGATTTGCAATTAACAAAGGGAATA 946
QY 956 AACTTAAATTATTAACAAAGTCAATGTAACAAAAATGATCTATTGATGAAATTTAA 1015
Db 947 TAAATTAAATTATTAACAAAAATTAATTAATGACAAAGTCAATTTGTTAATGATGAA 1006
QY 1016 TGAATTAACGAACAGTCAATTAACAAATTAACAAATTAACAAATTAACAAATTA 1048

```



```

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/180,209B
FILING DATE: 11-JAN-1994
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/031,400
FILING DATE: 11-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-074 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1341 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 153..1052
US-08-180-209B-26

```

```

Query Match      40.7%; Score 426.2; DB 1; Length 1341;
Best Local Similarity 66.9%; Pred. No. 3,7e-103;
Matches 660; Conservative 0; Mismatches 308; Indels 19; Gaps 3;

```

```

QY 64 CCGAGTTGACTTTTATGAGAAAGATATGATTTCTATGTTTACTCAAGGATTAAGCA 123
DB 156 CCCAATGTCCTTTTAACTCTGATACAGTTTCGATTAATTGAAACAGGAAACCGCA 215
QY 124 GATGGATTAATCTTTAAGAAAGAACTTTAAGSAATTAAGACTGTTTCAAAAGCTTACA 183
DB 216 AATCGATCTTTTATACACTACAGACATTAACAAATCACTGAAATTAAGAAAAAACT 275
QY 184 ATATCAAAACAAGTTGATTTCTTATACAGTGTTCCTTCAACTGGGAATATGAAAC 243
DB 276 ATBACACGTCAGTTGATTTATCAATACATGTTTACTTCACTCCAGAGTGAACAAAT 335
QY 244 TTCGTTGCTATGTCGAAAGCTTTAATGAAAAAGATGATTTCTGTAATTTGCGTGCAC 303
DB 336 TTCATTAATTTAGCAAAAGCTTTGATGATTAAGATTAATGATGTTATCTCAATCGAT 395
QY 304 TGGAGAAAGGTCCTGTAATGCTTTTGTCAACAAAGAGTCCTGGGATTTATCCAA 363
DB 396 TGGCAGACGCTGCTGTACTAATGAAAGCTGAGGTTTAAAGTATTATATCTCTACT 455
QY 364 GCCGTTGGAACAACAGTCAGTCGTTGGAATTTGTAGCTGATTTTCAAAACTACTTGT 423
DB 456 GCTGCTAGAAAATACAGTTTATGTTGACATATATGCTACATTAACCAAGAACTCGTA 515
QY 424 GAAAAATATTAAGTGTGATATCAATATACATGATGAGGAGTATGTTGGCGCGCAT 483
DB 516 AAAACCTATTAATCTCGATGCAATATATACATTAATGACATGCTAGAGACAT 575
QY 484 ACTTCAGTTTGGCGGAAAGAGTTCAAAAGTTTAAATTTGAAAAATACAGAAAT 543
DB 576 GCTTACAGTTTTCAGGCAAAAGTTTCAAGATTAAATTAAGAAAAATATCTGAAT 635
QY 544 ATCGGCTTGATCTGCTGAGACGTAATTTTCAATCGAGTACGTCGCGACAGACTTTC 603
DB 636 ATTGGCTTGATCTGCTGAGGCTTGTGATCAATCAATTTGTTCCGAAAGACTCTGC 695
QY 604 GTAACAGACGCAATATGTTCAAGTTATACATCAATCAATATTTAGAGATATAT 663

```

```

DB 696 GAGACAGATGCAGATATGTTCAAAATATATACATCACTAATTTAGAACCCAAAA 755
QY 664 AATGTTGAGAGTTGATTTTCACTGAAATTAATGAAAAAATCAACCTGTTGCAATGA 723
DB 756 ACCCTGTGACCGTGATTTTCAATGAATTAACGAAAGATCAACCTGTTGCGGTAGA 815
QY 724 CCATCC-----TGCTCTCATGAAAGCCGTAATATCTGAGTGCATTAATA 774
DB 816 TTTTCTCAGAGTTTGTCTCTCATTCGAGAGCCGATATACATGCTGAGTGCATTAATA 875
QY 775 CATGAATGTTGTTAATGGAACACCATGAAAGAAATATTCAGACTCCAAACCAAT 834
DB 876 CACGAATGTTGTTAATGAGATACC-----GAAGTCAAAAGTTCCGACGCTAAT 926
QY 835 TCCAGTGAGAGAGACACCTGTTGCGTTGATTAATGAATGAATTAATCTGCT 894
DB 927 TCGTGTCACAAAACAGAGAGTCGTTGCGTTGATTAATGAATGAATGAATGATCTG 986
QY 895 AGAGCGCATTTTATGACCCGTTGAGCAATATGACCTTATGCTATACAGAGGAGAT 954
DB 987 AGAGCTATTTTATGTAACCGTTGAAAGTACTGTTCTTTTGCATTAACAGGGAAG 1046
QY 955 AACTTTAATTAACAAAGTCAATGATACAAAAATATCTATGATGATTAATTA 1014
DB 1047 ATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1105
QY 1015 ATGAATTAACGACAGTCAAAATTAATA 1041
DB 1106 ATGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1132

```

```

RESULT 10
US-08-385-745-26
Sequence 26, Application US/08385745
Patent No. 5612209

```

```

GENERAL INFORMATION:
APPLICANT: King, Te Piao
TITLE OF INVENTION: Cloning and Recombinant Production of
TITLE OF INVENTION: Vespid Venom Phospholipases, and Immunological Therapies
TITLE OR INVENTION: Based Thereon
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESSES:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/385,745
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US/08/031,400
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 3288-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1341 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

```

TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 153..1052  
 US-08-385-745-26

Query Match 40.7%; Score 426.2; DB 1; Length 1341;  
 Best Local Similarity 66.9%; Pred. No. 3,7e-103;  
 Matches 660; Conservative 0; Mismatches 308; Indels 19; Gaps 3;

```

QY 64 CCGGATTGCTATTATATGAGAAAGATATAGTATTCATGTTTACTCAAGGATTAAGCGA 123
    |||
DB 156 CCCAATGTCCTTTTATTTCTGATACAGTTTCGATATATTGAAACAGGAAAAACCGA 215
    |||
QY 124 GATGTATTATTTCTTAAAGAAAGAACTTTAAGCAATTCGATCTGTTTCAAGGTCTACA 183
    |||
DB 216 AATCGTATCTTATACACTACAGACATACAGATCATCTGAATTTAAGAAAAAACT 275
    |||
QY 184 ATATCAAAACAATTGATTTCTTATACATGTTTCTTCACTGGGATTAATGAAGAC 243
    |||
DB 276 ATACACGTCAGTGTATTCATTAACATGTTTATCTTCATCTGCAGTGAACAAAT 335
    |||
QY 244 TTGCTGCTATGTCGAAAGCTTTAATAGAAAGATATTTCTGTAATTTGCGTGCAC 303
    |||
DB 336 TTCTAATATTTACGAAAGCTTTGTRGATTAAGATACATATGTTATCTCAATCGAT 395
    |||
QY 304 TGGAGAGAGGTCCTGTAAATGCTTTGCTTCAAGAAAGATCTTGGTTATTCGAA 363
    |||
DB 396 TGGCAGACGGCTGCTGTACTATGAAGCTGCAGGTTTAAAGTATTTATTTCTACT 455
    |||
QY 364 GCGGTTGGAACACAGTCACGTTGGAATTTGTAGCTGATTTTACAAACATCTGTA 423
    |||
DB 456 GCTGCTAGAAATACAGTTAGTGAACATTAATGCTACGATTCACGAAACCTGTA 515
    |||
QY 424 GAAAAATATTAAGTGCATATCAAAATATACGATTCGCGGATAGTTGGCGCGCAT 483
    |||
DB 516 AAACATCTTAATCTCGATGCGAATATACGATTAATGGAACATGACTTGAAGACAT 575
    |||
QY 484 ACTTCAGGTTTTCGCGAAAGAAAGTTCAAAAGTTAAATTTAGGAAATACAAAGAAAT 543
    |||
DB 576 GCTTCAGGTTTTCAGGCAAAAAGTTCAAGATTAATTTAGGAAAAATTTCTGAAT 635
    |||
QY 544 ATGCGGCTGATCTCTGTCGACCGTATTTTCAATCGAGTACGTCGCGACATCTTGC 603
    |||
DB 636 ATGCGGCTGATCTCTGTCGACCGTATTTTCAATCGATTCGATTCGCGAAACCTCTGC 695
    |||
QY 604 GTAAACAGACGCAATATGTTCAAGTTATACATCAATCAATCATATTAGAGATATTTAT 663
    |||
DB 696 GAGACAGATGCAAAATATGTTCAAAATTAATACATCAATCAATTAATTTAGAACCGAAAA 755
    |||
QY 664 AATGTTGTAGCGTTGATTTCTACGTAATTAAGAAAAAATCAACTGTTGCAATGAA 723
    |||
DB 756 ACCCTTGTATCGTTCGATTTCTACATGAATTAAGGAAAGATCAACTGTTGCGGTAGA 815
    |||
QY 724 CCATCC-----TGCTCTACATAGAAAGCCGTGAATATCTGACTGATGCAATAAA 774
    |||
DB 816 TTTTCTCAGAAAGTTGCTCTCAATCGAGCCGTGATTAACATGCTGATGCAATAAA 875
    |||
QY 775 CATGAATGTTGTTAATTTGGAACACCATGGAAGAAATATTTCGACCTCCAAAAACAAT 834
    |||
DB 876 CAGCAATGTTGTTAATTTGGAATACC-----GAGTCAAAAGGTTGCGACCTATT 926
    |||
QY 835 TCCCATGTCAGAGAGACACTGTGTTTGGTGGATGATGCAAAAGTTATCTCTCT 894
    |||
DB 927 TCGTGTGCACAAAACGAGAGTCGTTGCTGATTAACGCAAAAGATATTAATCTAGT 986
    |||
QY 895 AAGAGGCACTTTATGACCGGTTGAAGCAATGCACTTATTCCTAATCAAGGGGATT 954
    |||
DB 987 AAGAGGCTCATTTATGACCGGTTGAAGATGCTTCCTTTTGCATTAACAGGGGAG 1046
    |||
QY 955 AAACCTTAATTAACAAAGTCAATGTACACAAAAATGATATCTATTGATGAATTTAA 1014
    |||

```

DB 1047 ATATTTAATTAATATAAAAAAGT-AAATTCATTCATCGAAATGCAATTTGTTAATGTGA 1105  
 QY 1015 ATGAATTAACGAACAGTCAATTAATAA 1041  
 DB 1106 ATGAATTAATTAACCAATTAACAAATTA 1132

## RESULT 11

US-08-485-388-26  
 Sequence 26; Application US/08485388  
 Patent No. 6270763

GENERAL INFORMATION:  
 APPLICANT: King, Te Piao  
 TITLE OF INVENTION: Cloning and Recombinant Production of  
 TITLE OF INVENTION: Vespid Venom Phospholipases, and Immunological Therapies  
 NUMBER OF SEQUENCES: 27  
 CORRESPONDENCE ADDRESSES:  
 ADDRESSEE: Klauber & Jackson  
 STREET: 411 Hackensack Avenue  
 CITY: Hackensack  
 STATE: New Jersey  
 COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/485,388

FILING DATE: 07-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/385,745

FILING DATE: 08-FEB-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/031,400

FILING DATE: 11-MAR-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
 NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-074 FWCA

TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201 487-5800

TELEFAX: 201 343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 1341 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 153..1052  
 US-08-485-388-26

Query Match 40.7%; Score 426.2; DB 3; Length 1341;  
 Best Local Similarity 66.9%; Pred. No. 3,7e-103;  
 Matches 660; Conservative 0; Mismatches 308; Indels 19; Gaps 3;

```

QY 64 CCGGATTGCTATTATATGAGAAAGATATAGTATTTCTATGTTTACTCAAGGATTAAGCGA 123
    |||
DB 156 CCCAATGTCCTTTTATTTCTGATACAGTTTGGATTAATTTGAAACAGGAAAAACCGA 215
    |||
QY 124 GATGTATTATTTCTTAAAGAAAGAACTTTAAGCAATTCGATCTGTTTCAAGGTCTACA 183
    |||
DB 216 AATCGTATCTTATACACTACAGACATTAAGCAATCATCTGAATTTAAGAAAAAACT 275
    |||

```

```

QY 184 ATATCAAAAGAGTTGATTTCTTATACAGTTTCTTCACTGGCAATATGAAAC 243
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 276 ATACAGCTGCGATTTATTCATACAGTTGTTTACTTCACTGCAAGTGAACAAAT 335
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 244 TTGCTGCTATGTCGAAGCTTTAATAGAAAAAGATGTTTCTGTAAATTCGTCAC 303
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 336 TTTCATTAATTTAGCAAAAGCTTTGTAGTAAAGATACATATATGTTATCTCAATCGAT 395
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 304 TGGAAAGAGGTCGTATATGCTTTTGTCAAGAAAGCTGTTGGTTATTCGAA 363
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 396 TGGCAACGCGTCTGTTACTAATAGAGTGCAGGTTTAAAGTATTTATATATCTTACT 455
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 364 GCGGTGAAACACACGTCACGTTGAAATTTAGTCTGATTTTCAAAACTACTTGT 423
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 456 GCTGTAGAAATACAGTTTATGTAACATATATGCTACATTTCCAGAAACCTCGTA 515
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 424 GAAAAATATTAAGTCTGATATTAATATACATTTGATGGGCTATGTTGGCGCGCAT 483
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 516 AAACCTATTAATCTCGATGCGAAATATACATTAATTTGACATGCTTAGGACGACAT 575
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 484 ACTTCAGTTTTCGGGAAAGAGTTCAAAAGTTAAATTTGGAATATACAGAAAT 543
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 576 GCTTCAGTTTTCAGGCAAAAGGTTCAAGGTTAAATTTAGAAATATTTCTGAAT 635
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 544 ATCGGCTGATCTCTGTCGACCGTATTTTCATCGAGTGACTGTCGACAGACTTTC 603
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 636 ATTGGCTTGATCTCTGTCGACCGTATTTTCATCGAGTGACTGTCGACAGACTTTC 695
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 604 GTTACAGACGCAAGATATGTTCAAGTTATACATCAATCAATCAATTTAGAGTATAT 663
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 696 GAGACAGATGCAAGATATGTTCAATTAATACATCAATCAATTTAGAGTATAT 755
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 664 AATGTTGAGGTTGATTTCTACGGAATTTAGAAAAATTAACCTGTTGCATGAA 723
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 756 ACCCTTGATCGTCAATTTCTACATGAATTAACGAAAGATCACTGTTGCGGTAGA 815
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 724 CCATCC-----TGCTCTACGAAAGCGTGAATATCTGAGTGCATGAA 774
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 816 TTTTCTCAGAAAGTTTGCTCTCATTTGAGAGCGGTGATATACAGTCTGAGTGCATGAA 875
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 775 CATGAATGTTGTTTAAATGGAACACCATGGAAGAAATTTTACGACTCCAAAACCAAT 834
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 876 CACGATGTTGTTTAAATGGAATAC-----GAGTCAAGAGTTGCGACGCTTAT 926
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 835 TCCCGATGAGAGACACCTGTTGTTGCTGATGATGAATGCAAAAAAGTATCTGCT 894
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 927 TCGTCTGACAAAGAGAGTGGCTTTGCTGATTAACGCAAGAAATGATATCTAGT 986
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 895 AAGGCGCATTTTATGACCGGTGAAGCAATGCACTTATGTCATACGAGGAGAT 954
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 987 AAGGCGCATTTTATGACCGGTGAAGTACGTTTCTTTTGAATTAACAGAGGAG 1046
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 955 AAACCTTATTTAAACAAAGTCAATGATACCAAAATGATCTATGATGAATTTAA 1014
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1047 ATTAATTTAATATATTAATAAGT-ATTTTCATTCATGCAAAATGATTTGTTAATGTGA 1105
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1015 ATGAATTAACGAACGTCATTAATAAA 1041
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1106 ATGAATTAATTAACATTTTAACAATTA 1132
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 12
US-08-474-853-26
; Sequence 26, Application US/08474853
; Patent No. 6287359
; GENERAL INFORMATION:
; APPLICANT: King, Te-piao
; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
; TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND
; TITLE OF INVENTION: HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED THEREON
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson

```

```

; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,853
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/180,209
; FILING DATE: 11-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/031,400
; FILING DATE: 11-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1341 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 153..1052
; US-08-474-853-26
;
Query Match 40.7%; Score 426.2; DB 3; Length 1341;
Best Local Similarity 66.9%; Pred. No. 3.7e-103;
Matches 660; Conservative 0; Mismatches 308; Indels 19; Gaps 3;

```

```

Db      576 GCTTCAGTTTTCAGGCAAAAAGTTCAAGATTAAATTTAGAAAATTTCTGAAATT 635
Qy      544 ATGGGCTTGATCTCTGTGAGACCGTATTTTCATCGAGTGACTGTCCGAGACAGCTTTC 603
Db      636 ATTGGCTTGATCTCTGTGAGACCGTATTTTCATCGAGTGACTGTCCGAGACAGCTTTC 695
Qy      604 GTAAACAGCCAGAAATTTTCAAGTTATATATATATATATATATATATATATATATAT 663
Db      696 GAGACAGATCAGAAATTTTCAATTTATATATATATATATATATATATATATATATAT 755
Qy      664 ATATGTTGATGCTGTTGATTTCTACGTAAATTAATGAAAAATCAACCTGGTGCATGAA 723
Db      756 ACCCTTGATACCGTCAATTTCTACATATATACGAAAGATCAACCTGGTGCATGAA 815
Qy      724 CCATCC-----TGCTCTCATACGAAAGCCGTGAATATCTGACTGAGTGATATAA 774
Db      816 TTTTTCAGAAAGTTTCTCTCATTCGAGGCGGTATATACATGCTGAGTGATATAA 875
Qy      775 CATGAATGTTGTTTATATTTGAAACCCATGAGAAATATTTCCACTCCAAACCAATT 834
Db      876 CAGAAATGTTTAAATTTGGAATACC-----GAAGTCAAGAGTTTGCAGCCTAATT 926
Qy      835 TCCAGTGCAGAGAGACACCTGTGTTGGTTGATTTGATGCAAAAAGTTATCTGCT 894
Db      927 TCCTGCTGCAAAAACAGAGTGGCTTTGGTTGATTTAAACGCAAGAAATATCTACT 986
Qy      895 AGAGGCGCATTTTATGACCGGTTGAAGCAATGCACTTATGCCATTAAGAGGGAAT 954
Db      987 AGAGGCTCATTTTATGTAACGGTTGAAGATAGTCTTTTGGCAATTAAGAGGGAAG 1046
Qy      955 AAATTTTATTTAAACAAAGTCAATGTAACAAAAATGATCTATTTGATGATTTAA 1014
Db      1047 ATATTTTAAATTAATATAAAAGT-ATTTTCATTCATCAAGAAATGATTTGTTATG 1105
Qy      1015 ATGAATTAACGAACTCAATTAATAA 1041
Db      1106 ATGAATTAATTAACATTTAAACAAATTA 1132

RESULT 13
US-09-166-205B-26
; Sequence 26, Application US/09166205B
; Patent No. 6372471
; GENERAL INFORMATION:
; APPLICANT: Te Piao KING
; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF VESPID VENOM ENZYMES,
; TITLE OF INVENTION: SUCH AS PHOSPHOLIPASE AND HYALURONIDASE, AND IMMUNOLOGICAL
; FILE REFERENCE: 2313/0F1380US
; CURRENT APPLICATION NUMBER: US/09/166,205B
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 1341
; TYPE: DNA
; ORGANISM: Vespula vulgaris
US-09-166-205B-26
```

```

Query Match      40.7%; Score 426.2; DB 3; Length 1341;
Best Local Similarity 66.9%; Pred. No. 3.7e-103;
Matches 660; Conservative 0; Mismatches 308; Indels 19; Gaps 3;

Qy      64 CCGAATGTAATTTTATGAGAAAGATATAGTATTTCTATGTTTACTCAAGGATTAAGCGA 123
Db      156 CCAATATGCTTTTATTTCTGATACAGTTTCGATATATTTGAAACAGGGAACCGA 215
Qy      124 GATGTAATTTCTTAAAGAAAGAACTTTAACAATTAAGATCTGTTTCAAAAGTCTACA 183
Db      216 AATCGATGATCTTTATCACTACAGACATTAACAATCATCTGAATTTAAGAAAAAAT 275
Qy      184 ATATCAAAACAATTTGATTTCTTATACATGTTTCTTCAACTGGAAATATGAAGAAC 243
```

```

Db      276 ATAAACAGTCAGTTGATTTATTTACATAGTGTTTTACTTCACTCGAAGTGAACAAAT 335
Qy      244 TTGCTGCTATGTCGAAGCTTTTAAATAGAAAAAGATATTTCTGTAATTTCCGTGCAC 303
Db      336 TTCAATTAATTTACAAAGCTTTTGTATGATTAAGAAATATATATATATATATATATAT 395
Qy      304 TGAAGAAAGGCTGCTGTAATGCTTTTGTCTTCAACAAAGATGCTTTGGTTATTTCCAA 363
Db      396 TGGCAGACGCTCTGTTATATGAAAGCTGACGTTTAAAGATTTATTTATTTCTACT 455
Qy      364 GCGGTGGAAGAACACGTCACGTGAAAAATTTGACGTGATTTTCAAAAGTACTGTA 423
Db      456 GCTGCTAGAAATACGTTTATGTTGACAAATATATCTGACATTCACCGAAGACATGTA 515
Qy      424 GAAAAATATTAAGTGTGATATCAAAATATACGATTTGATCGGGCATATGTTGGCGCAT 483
Db      516 AAACATATTAATTTCTGATGCAATTAATGCAATTAATTTGACATATGCTTAGAGACAT 575
Qy      484 ACTTCAGTTTTCGGGAAAAAGATTCAAAAGTTAAATTTAGAAATATCAAGAAATTT 543
Db      576 GCTTCAGTTTTCAGGCAAAAAGTTCAAGATTAATTAAGAAATATTTCTGAATTT 635
Qy      544 ATGGGCTTGATCTCTGTGAGACCGTATTTTTCATCGAGTGACTGTCCGAGACAGCTTTC 603
Db      636 ATGGGCTTGATCTCTGTGAGACCGTATTTTTCATCGAGTGACTGTCCGAGACAGCTTTC 695
Qy      604 GTAAACAGCCAGAAATATGTTCAAGTTATATACATATCAATCATATTTAGAGATATATT 663
Db      696 GAGACAGATGCAAAATATGTTCAAAATTTATATATATATATATATATATATATATATAT 755
Qy      664 ATATGTTGATGCTGTTGATTTCTACGTGAATTAATGAAAAATCAACCTGGTGCATGAA 723
Db      756 ACCCTTGTAACCGTCAATTTCTACATGAATTAACGAAAGATCAACCTGGTGCATGAA 815
Qy      724 CCATCC-----TGCTCTCATACGAAAGCCGTGAATATCTGACTGAGTGATATAA 774
Db      816 TTTTTCAGAAAGTTTCTCTCATTCGAGGCGGTATATACATGCTGAGTGATATAA 875
Qy      775 CATGAATGTTGTTTAAATTTGAAACCCATGGAAGAAATATTTTCAGACTCCAAACCAATT 834
Db      876 CAGAAATGTTGTTTAAATTTGGGATACC-----GAAGTCAAGAGTTTGCAGCCTAATT 926
Qy      835 TCCAGTGCAGAGAGACACCTGTGTTGGTTGATTTGATGCAAAAAGTATCTGCT 894
Db      927 TCCTGCTGCAAAAACAGAGTGGCTTTGGTTGATTTAAACGCAAGAAATATCTACT 986
Qy      895 AGAGGCGCATTTTATGACCGGTTGAAGCAAAATGCACTTATGCAATAAGAGGGAAT 954
Db      987 AGAGGCTCATTTTATATGACCGGTTGAAGATAGTCTTTTGGCAATTAACAGGGAAG 1046
Qy      955 AAATTTTATTTAAACAAAGTCAATGTAACAAAAATGATCTATTTGATGATTTAA 1014
Db      1047 ATATTTTAAATTAATATAAAAGT-ATTTTCATTCATCAAGAAATGATTTGTTATG 1105
Qy      1015 ATGAATTAACGAACTCAATTAATAA 1041
Db      1106 ATGAATTAATTAACATTTAAACAAATTA 1132
```

```

RESULT 14
PCT-US94-02629-26
; Sequence 26, Application PC/TUS9402629
; GENERAL INFORMATION:
; APPLICANT: King, Te-Piao
; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
; TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND
; TITLE OF INVENTION: HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED THEREON
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
```

```

STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/02629
FILING DATE: 10-MAR-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/180,209
FILING DATE: 11-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/031,400
FILING DATE: 11-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-074 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1341 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 153..1052
PCT-US94-02629-26

```

```

Query Match      40.7%; Score 426.2; DB 5; Length 1341;
Best Local Similarity 66.9%; Pred. No. 3.7e-103;
Matches 660; Conservative 0; Mismatches 308; Indels 19; Gaps 3;

```

```

QY 64 CCGAGTTGCTTTTAAAGAGAAATATATCTATGTTTACTCAAGGATAGCGA 123
DB 156 CCGAATGCTTTTAAATCTGATACAGTTGATTAATTAAGAAAGGAAACCGA 215
QY 124 GATGCTATTTCTTAAGAAAGAACTTTAAGCAATGCTGTTTCAAAAGCTACA 183
DB 216 AATCGGATCTTTATACACTACAGACATTAAGAAATCATCTGAATTTAAGAAAAAACT 275
QY 184 ATATCAAAACAGTTTATTTCTTATACAGGTTTCTTCACTGGAAATATGAAGC 243
DB 276 ATBACGCTCCAGTTTATTTCACTACATGTTTACTTCACTGCAAGTGAACAAT 335
QY 244 TTGCTGCTATGTCGAAGCTTTAATAGAAAAAGATGTTTCTTGAATTTGCTGAC 303
DB 336 TTCATTAATTTGCAAAAGCTTTGTAAGTAAGAAATTAATGTTTCAATTCAT 395
QY 304 TGAAGAAAGGCTGCTGTAATGCTTTGCTTCAAGAAAGATGCTTTGGGTTATTCAAA 363
DB 396 TGGCAGACCGCTGCTTACTATGAAAGCTGCAAGTTTAAAGATTTATATCTTACT 455
QY 364 GCGGTTGGAACACAGTCAGCTTGAATTTGTAGCTGATTTTACAAACTACTGTGA 423
DB 456 GCTGCTAGAAATACAGTTTATGTTGACATATATGCTACATTAACCAAGAACTCGTA 515
QY 424 GAAAAATATAAAGTGTATATCAATATACATGATGCGGATAGTTGGCGCGCAT 483
DB 516 AAACACTAATAAATCGATGGAATATACGATTAATGACATATGCTTAGAGACAT 575
QY 484 ACTTCAAGTTTGGCGGAAAGAGTTCAAAAGTTAAATTTAGAAATTAACAAGAAAT 543
DB 576 GCTTCAAGTTTGGCGGAAAGAGTTCAAGAGTTAAATTTAGAAATATCTGAAAT 635

```

```

QY 544 ATCGGCTTGATCTGCTGAGACCGATTTTCAATGGAAGTACGTCCGAGACACTTGC 603
DB 636 ATTTGGCTTGATCTGCTGAGACCGCTTCTGATTAATCAATCTTTCCAAAGACTTGC 695
QY 604 GTAACAGACGCAATATGTTCAAGTTATACATCATCAATATTAAGATATATAT 663
DB 696 GAGACAGATGCAAAATATGTTCAATTTATACATCAATCAATATTTAGAACCGAAAA 755
QY 664 AATGTTGTAAGCTGTTTCTACGTGAATTAATGAAAAAATCAACTGTTGCAATGA 723
DB 756 ACCCTTGTAACGTCGATTTCTACATGAATACGAAAGAAATCAACTGTTGCGGTGA 815
QY 724 CCATCC-----TGCTCTATGCAAGCCGTAATATCTGACGAGTCAATAAA 774
DB 816 TTTTCTCAGAAAGTTGCTCTTCAATTCGAGCCGTAATATACATGCTGAGTCAATAAA 875
QY 775 CATGAATGTTTATTAATGGAACACCATGGAAGAAATATTTGAGCACTCCAAACCAAT 834
DB 876 CACGAATGTTTATTAATGGAATACC-----GAAGTCAAGAGTTCCGAGCTATTT 926
QY 835 TCCAGTGCAGAGGACACCTGTTGCTGCTGATGATGCAAAAAGTTATCTGCT 894
DB 927 TCGCTGCACAAAACAGAGTGCCTTGCCTTGATTAACGCAAGAGTATCTAGT 986
QY 895 AGAGGCGATTTATGACCCGCTTGAGCAAAATGACCTTATGTCATTAAGAGGAGATT 954
DB 987 AAGGCTATTTTATTAATGACCGCTTGAAGTACGTTCTTTTGCATTAACAGGGAAG 1046
QY 955 AAATTTAATTAATAACAAAGTCAATGTAACAAAAATGATCTTAATGATGAATATTA 1014
DB 1047 ATTAATTAATTAATAAAAAAGT-AAATTCATTCATGAATGATGATTTGTTAATGTTGA 1105
QY 1015 ATGAATTAACGAACGCTCAATTAATA 1041
DB 1106 ATGAATTAATTAACCAATTAACAAATTA 1132

```

```

RESULT 15
US-09-806-708B-22
Sequence 22, Application US/09806708B
Patent No. 6784342
GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
FILE REFERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US/09/806,708B
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/147,133
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patent in version 3.0
SEQ ID NO 22
LENGTH: 1141
TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
NAME/KEY: promoter
LOCATION: (1)..(1141)
OTHER INFORMATION: consensus sequence of A.C., L.a., and B.n. PAB1 promoters
US-09-806-708B-22

```

```

Query Match      5.6%; Score 59; DB 4; Length 1141;
Best Local Similarity 12.5%; Pred. No. 8.8e-06;
Matches 131; Conservative 357; Mismatches 552; Indels 5; Gaps 2;

```

```

QY 1 ATTTGCTTCTTGATGATGATTCAGACATTTAGAAATGTAATGATGAGGAGATG 60
DB 91 ANNISBRHARWKMKTAAYEMTNNKXGKQWRHRYRWRAMBTDVHHVYTAANNMT 150
QY 61 TCTCCGAAATGTTACTTTTAATGAGAAAGATATAGTATTTCTACTCAAGGATAG 120
DB 151 TWCMDKDKETRWKKNNNATGWDDBDTKYHMMNNNCBVTVMVRYKTRDWSBKMN 210

```





**THIS PAGE LEFT BLANK**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 28, 2005, 21:42:49 ; Search time 731 Seconds  
(without alignments)  
8727.627 Million cell updates/sec

Title: US-10-688-011-1  
Perfect score: 1048  
Sequence: 1 atttgcttcttgtagatga.....agtcacataaaaaaaaaa 1048

Scoring table:  
IDENTITY\_NUC  
Gap 10.0 , Gapext 1.0

Searched: 5642217 seqs, 3043843248 residues

Total number of hits satisfying chosen parameters: 11284434

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:  
1: /cgn2\_6/prodata/1/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/prodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/prodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/prodata/1/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/prodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/prodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/prodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/prodata/1/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/prodata/1/pubpna/US09A\_PUBCOMB.seq:\*  
10: /cgn2\_6/prodata/1/pubpna/US09B\_PUBCOMB.seq:\*  
11: /cgn2\_6/prodata/1/pubpna/US09C\_PUBCOMB.seq:\*  
12: /cgn2\_6/prodata/1/pubpna/US09C\_NEW\_PUB.seq:\*  
13: /cgn2\_6/prodata/1/pubpna/US10A\_PUBCOMB.seq:\*  
14: /cgn2\_6/prodata/1/pubpna/US10B\_PUBCOMB.seq:\*  
15: /cgn2\_6/prodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
16: /cgn2\_6/prodata/1/pubpna/US10D\_PUBCOMB.seq:\*  
17: /cgn2\_6/prodata/1/pubpna/US10E\_PUBCOMB.seq:\*  
18: /cgn2\_6/prodata/1/pubpna/US10F\_PUBCOMB.seq:\*  
19: /cgn2\_6/prodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
20: /cgn2\_6/prodata/1/pubpna/US11\_NEW\_PUB.seq:\*  
21: /cgn2\_6/prodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
22: /cgn2\_6/prodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1048	100.0	1048	18	US-10-688-011-1
2	49.2	4.7	460	9	US-09-960-352-12840
3	48.6	4.6	3673778	16	US-10-312-841-1
4	47	4.5	3564	19	US-10-741-600-478
5	46.8	4.5	1526	17	US-10-398-663-12
6	46.8	4.5	3635	14	US-10-116-802-28
7	46.2	4.4	13326	15	US-10-311-455-1686
8	45.8	4.4	7786	9	US-09-790-988-2
9	45.6	4.4	1605	9	US-09-917-800A-1549
10	45.2	4.3	1383	17	US-10-312-088-1
11	45.2	4.3	1401	16	US-10-403-745-2

12	45.2	4.3	1404	13	US-10-038-517-1	Sequence 1, Appl1
13	45.2	4.3	2352	16	US-10-403-745-1	Sequence 1, Appl1
14	45.2	4.3	3549	9	US-09-954-456-2217	Sequence 2217, Ap
15	45.2	4.3	3549	10	US-09-802-640-13	Sequence 13, Appl
16	45.2	4.3	3549	17	US-10-403-902A-13	Sequence 13, Appl
17	45.2	4.3	3549	18	US-10-755-889-99	Sequence 99, Appl
18	45.2	4.3	3549	18	US-10-789-378-47	Sequence 47, Appl
19	45.2	4.3	3549	19	US-10-843-641A-5244	Sequence 5244, Ap
20	45.2	4.3	4075	10	US-09-971-392-107	Sequence 107, Appl
21	45.2	4.3	4314	18	US-10-723-860-6562	Sequence 6562, Ap
22	45	4.3	3184	9	US-09-934-268-1	Sequence 1, Appl1
23	45	4.3	3184	14	US-10-162-435-35	Sequence 35, Appl
24	45	4.3	3184	19	US-10-860-779-35	Sequence 960, Appl
25	44.6	4.3	17294	15	US-10-311-455-960	Sequence 960, Appl
26	44.4	4.2	421	9	US-09-960-352-8123	Sequence 8123, Ap
27	44.4	4.2	453	9	US-09-960-352-1906	Sequence 1906, Ap
28	44.4	4.2	1603	10	US-09-802-640-19	Sequence 19, Appl
29	44.4	4.2	1603	17	US-10-403-902A-19	Sequence 19, Appl
30	44.4	4.2	1603	18	US-10-335-053-235	Sequence 235, Appl
31	44.2	4.2	1767	16	US-10-349-680-163	Sequence 163, Appl
32	44.2	4.2	8634	15	US-10-311-455-1029	Sequence 1029, Ap
33	44.2	4.2	17389	15	US-10-311-455-1387	Sequence 1387, Ap
34	44	4.2	333	18	US-10-357-930-12856	Sequence 12856, A
35	43.8	4.2	16688	15	US-10-311-455-294	Sequence 294, Appl
36	43.6	4.2	433	18	US-10-425-115-12621	Sequence 12621, A
37	43.6	4.2	14112	15	US-10-311-455-1416	Sequence 1416, Ap
38	43.6	4.2	14112	17	US-10-221-714A-200	Sequence 200, Appl
39	43.6	4.2	14112	18	US-10-433-793-10	Sequence 10, Appl
40	43.4	4.1	5857	15	US-10-311-455-502	Sequence 502, Appl
41	43.2	4.1	481	18	US-10-437-963-78790	Sequence 78790, A
42	43.2	4.1	1530	19	US-10-741-600-750	Sequence 750, Appl
43	43.2	4.1	1659	19	US-10-741-600-751	Sequence 751, Appl
44	43.2	4.1	1975	18	US-10-425-115-80851	Sequence 80851, A
45	43.2	4.1	6109	15	US-10-311-455-239	Sequence 239, Appl

## ALIGNMENTS

RESULT 1  
US-10-688-011-1  
; Sequence 1, Application US/10688011  
; Publication No. US20040175393A1  
; GENERAL INFORMATION:  
; APPLICANT: King, Te Piao  
; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF POLISTINE VENOM ENZYMES,  
; TITLE OF INVENTION: SUCH AS PHOSPHOLIPASE AND HYALURONIDASE, AND IMMUNOLOGICAL  
; TITLE OF INVENTION: THERAPIES BASED THEREON  
; FILE REFERENCE: 02313/100F138-US2  
; CURRENT APPLICATION NUMBER: US/10/688, 011  
; PRIOR FILING DATE: 2003-10-17  
; PRIOR APPLICATION NUMBER: US 09/806, 658  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: PCT/US99/23211  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: US 09/166, 205  
; PRIOR FILING DATE: 1998-10-01  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 1048  
; TYPE: DNA  
; ORGANISM: Polistes annularis  
US-10-688-011-1  
Query Match 100.0%; Score 1048; DB 18; Length 1048;  
Best Local Similarity 100.0%; Pred. No. 1.6e-234;  
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATTGCTTCTTGTAATGATTCGACGACATTGAAATGTAACCTTGATAGAGCATG 60  
Db 1 ATTGCTTCTTGTAATGATTCGACGACATTGAAATGTAACCTTGATAGAGCATG 60

```

QY 61 TCTCCGAAATGTAATCTTTAATGAGAAAGATATAGTATCTATGTTTACTCAAGGATTAAG 120
    |||
DB 61 TCTCCGAAATGTAATCTTTAATGAGAAAGATATAGTATCTATGTTTACTCAAGGATTAAG 120
QY 121 CGAGATGATTAATCTTTAAGAAAGAACTTTAAGCAATTCATCTGTTTACAAAGTCT 180
    |||
DB 121 CGAGATGATTAATCTTTAAGAAAGAACTTTAAGCAATTCATCTGTTTACAAAGTCT 180
QY 181 ACAATATCAAAAACAAGTGAATCTTATATCATGATGTTTCTTCAACTGGGAAATATGAA 240
    |||
DB 181 ACAATATCAAAAACAAGTGAATCTTATATCATGATGTTTCTTCAACTGGGAAATATGAA 240
QY 241 AACTGCTGCTATGTCGAAAGCTTTAATAGAAAAAGATGATTTCTGTATTTGCGTC 300
    |||
DB 241 AACTGCTGCTATGTCGAAAGCTTTAATAGAAAAAGATGATTTCTGTATTTGCGTC 300
QY 301 GACTGGAAGAGGGTCTGTGTAATGCTTTGCTTCAACAAGAGTCTTTGGTTATTC 360
    |||
DB 301 GACTGGAAGAGGGTCTGTGTAATGCTTTGCTTCAACAAGAGTCTTTGGTTATTC 360
QY 361 AAAGCGGTTGGAACAACAGTCAGTTGGAATTTGATGCTGATTTTCAAAACTACTT 420
    |||
DB 361 AAAGCGGTTGGAACAACAGTCAGTTGGAATTTGATGCTGATTTTCAAAACTACTT 420
QY 421 GTAGAAAAATATTAAGTGTGATATCAAAATATACATGATCGGCAATGTTGGCGCG 480
    |||
DB 421 GTAGAAAAATATTAAGTGTGATATCAAAATATACATGATCGGCAATGTTGGCGCG 480
QY 481 CATACTTCAGGTTTGGCGGAAAAAGATCAAAAGTTAAATTAGAAAAATACAGAA 540
    |||
DB 481 CATACTTCAGGTTTGGCGGAAAAAGATCAAAAGTTAAATTAGAAAAATACAGAA 540
QY 541 ATTATCGGGCTTATCTGCTGGAACCGTATTTTCATCGAGTACGTCGCGACAAT 600
    |||
DB 541 ATTATCGGGCTTATCTGCTGGAACCGTATTTTCATCGAGTACGTCGCGACAAT 600
QY 601 TGGGTAAACAGACGACAGATATGTTCAAGTTATACATACATCATATTTAGAGATAT 660
    |||
DB 601 TGGGTAAACAGACGACAGATATGTTCAAGTTATACATACATCATATTTAGAGATAT 660
QY 661 TATTAATGTTGTTGCGTGTGATTTCTACGTAATTAAGAAAAATCACTGGTTGCAAT 720
    |||
DB 661 TATTAATGTTGTTGCGTGTGATTTCTACGTAATTAAGAAAAATCACTGGTTGCAAT 720
QY 721 GAACCATCTCTGCTGATACGAAAGCGGAAATATCTGAGTGCATTAACATGAA 780
    |||
DB 721 GAACCATCTCTGCTGATACGAAAGCGGAAATATCTGAGTGCATTAACATGAA 780
QY 781 TGTGTTTATTTGGAACACCATGGAAGAAATATTTGAGCATCTCCAAACCAATTTCCAG 840
    |||
DB 781 TGTGTTTATTTGGAACACCATGGAAGAAATATTTGAGCATCTCCAAACCAATTTCCAG 840
QY 841 TGCAGAGAGACACCTGTGTTTGGTTCGTTGATGCAAAAAGTTATCTGCTAGAGC 900
    |||
DB 841 TGCAGAGAGACACCTGTGTTTGGTTCGTTGATGCAAAAAGTTATCTGCTAGAGC 900
QY 901 GCATTTTATGACACCGGTTGAGCAATGACCTTATTTGCAATACAGGGGATTAACCT 960
    |||
DB 901 GCATTTTATGACACCGGTTGAGCAATGACCTTATTTGCAATACAGGGGATTAACCT 960
QY 961 TAAATTAATAACAAAGTCAATGATACAAAAATGATCTATGATGATTAATTAATGAAT 1020
    |||
DB 961 TAAATTAATAACAAAGTCAATGATACAAAAATGATCTATGATGATTAATTAATGAAT 1020
QY 1021 AAAACGACGCTCAATTAATAATAATAATAATAATAATAATAATAATAATAATAATA 1048
    |||
DB 1021 AAAACGACGCTCAATTAATAATAATAATAATAATAATAATAATAATAATAATAATA 1048

```

RESULT 2  
 US-09-960-352-12840  
 ; Sequence 12840, Application US/09960352  
 ; Patent No. US20020137139A1

```

; GENERAL INFORMATION:
; APPLICANT: Warren, Wesley C.
; APPLICANT: Tao, Nengping
; APPLICANT: Byatt, John C.
; APPLICANT: Mathialagan, Nagappan
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
; FILE REFERENCE: 16511.006/37-21(10298)C
; CURRENT APPLICATION NUMBER: US/09/960,352
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 15112
; SEQ ID NO 12840
; LENGTH: 460
; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 55-LIB2809-014-Q1-E1-F4
US-09-960-352-12840

```

Query Match 4.7%; Score 49.2; DB 9; Length 460;  
 Best Local Similarity 51.4%; Pred. No. 0.25;  
 Matches 148; Conservative 0; Mismatches 128; Indels 12; Gaps 1;

```

QY 359 CCAAGCCGTTGGAAACACACGTCACGTTGAAAAATTTGAGCTGATTTTACAAACTAC 418
    |||
DB 3 CCAAGCCGCGGGATACACCAAGCTGTGGACAGAGATGTGCCAAGTTTATGAACCTGA 62
QY 419 TTGTAGAAAAATTAAGTGTGATATCAAAATATACATGATTCGGCATATGTTGGCGG 478
    |||
DB 63 TGGCGGATGAATTTTAATCTATCTCCCTGGCAATGTGATCTTTGGATACACCTTGGGG 122
QY 479 CCCATCTTCAGGTTTGGCGGAAAAAGATCAAAAGTTAAATTAGAAAAATACAG 538
    |||
DB 123 CCCATCTCTGCTGATTTGAGGAGATCTGACCAATAG-----AAGTCAACA 170
QY 539 AAATTAATCGGGCTTATCTGCTGACCGTATTTTCATCGAGTACGTCTCGACAGC 598
    |||
DB 171 GGAATACCGGCTTAGATCCAGCTGACCTTAACCTTGAGATGACAGAGCTCCAAGTCCG 230
QY 599 TTGGGTAAACAGACGACAGATATGTTCAAGTTATACATACATCAATCA 646
    |||
DB 231 TTCTCTGATGATGGGATTTTGTAGAGTTTACACATTCACCA 278

```

RESULT 3  
 US-10-312-841-1/C  
 ; Sequence 1, Application US/10312841  
 ; Publication No. US20030186277A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Epigenomics AG  
 ; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC  
 ; FILE REFERENCE: E01/1208/NO  
 ; CURRENT APPLICATION NUMBER: US/10/312,841  
 ; CURRENT FILING DATE: 2002-12-30  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SEQ ID NO 1  
 ; LENGTH: 3673778  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
 ; NAME/KEY: unsure  
 ; LOCATION: (3294164)  
 US-10-312-841-1

Query Match 4.6%; Score 48.6; DB 16; Length 3673778;  
 Best Local Similarity 54.9%; Pred. No. 21;  
 Matches 96; Conservative 0; Mismatches 79; Indels 0; Gaps 0;

```

QY 874 AATGAAAAAGTTATCTGCTAGAGCGCATTTTATGACCGGTTGAAGCAAAATGCACCT 933
    |||
DB 3246566 AAAATTAATAATTAATACTTAACATCAATTTCTATCCCACTAAATGATAAACAAA 3246507

```

QY 934 TATGCATACGAGGGGATTAACCTTAATTAATAACAAAGTCATGTACACAAAT 993  
 Db 3246506 AATTCAACTACATTAATACTTAATAATAAAAAAAAAAAAAAAAAA 3246447  
 QY 994 GTATCTATGTAGTAATTAATTAATGAATAAAGACAGCTCAATTAATAAAAA 1048  
 Db 3246446 ATTAACATTTCTTTAAAAAATTAATAATAAAAAAAAAAAAAAAAAA 3246392

RESULT 4  
 US-10-741-600-478  
 ; Sequence 478, Application US/10741600  
 ; Publication No. US2005026169A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CARGILL, Michele et al.  
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
 ; FILE REFERENCE: CLO01499  
 ; CURRENT APPLICATION NUMBER: US/10/741,600  
 ; NUMBER OF SEQ ID NOS: 73997  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 478  
 ; LENGTH: 3564  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)...(3564)  
 ; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-  
 US-10-741-600-478

Query Match 4.5%; Score 47; DB 19; Length 3564;  
 Best Local Similarity 50.7%; Pred. No. 2.1;  
 Matches 144; Conservative 1; Mismatches 127; Indels 12; Gaps 1;

QY 365 CCGTGGAAACACACGTCAGCTGGAAATTTGAGCTGATTTTACAAACTTCTGTAG 424  
 Db 559 CCGCGGCTACACCAACCTGGTGAGACAGATGNGCCGTTTATCACTGATGAGG 618  
 QY 425 AAAAATATAAGTCTGATATCAATATATGATTCGAGCTAGTTGGCGCGCAT 484  
 Db 619 AGGARTTAATCTACCTCTGACATGTCCATCTCTGGATACAGCTTGAGCCATG 678  
 QY 485 CTTCAGGTTTGGCGGAAAAAGATTCAAAAGTTAAATTAGAAATACAGAAATTA 544  
 Db 679 CTGCTGGCATTTGACGAGAGCTGACCAATTAAG-----AAAGTCAAGAAATTA 726  
 QY 545 TGGGGCTTATCTGCTGAGCGGATTTTTCATGCGAGTCACTGTCGGAAGACTTTGGC 604  
 Db 727 CTGGCTTCGATCCAGCTGAGCTTAACCTTGAATGACAGAGCCCGAGTGTCTTCTC 786  
 QY 605 TTAACAGCAGCATATGTTCAAGTTATATACATCATCATCAT 648  
 Db 787 CTGATGATGCAATTTTGTGACGTCTTACACACATTCACACAGA 830

RESULT 5  
 US-10-398-663-12  
 ; Sequence 12, Application US/10398663  
 ; Publication No. US20040053281A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: INCYTE, CORPORATION; HARLAND, Lee;  
 ; APPLICANT: ARVIZU, Chandra S.; DAS, Debopriya;  
 ; APPLICANT: GRIFPIN, Jennifer A.; BAUGHN, Mariah R.;  
 ; APPLICANT: DING, Li; CHAMLA, Narinder K.;  
 ; APPLICANT: YAO, Monique G.; LU, Yan;  
 ; APPLICANT: ELLIOTT, Vicki S.; THANGAVELU, Kavitha;  
 ; APPLICANT: RAMKUMAR, Udayakumari; LAL, Preeti G.;  
 ; APPLICANT: TRIBOULEY, Catherine M.  
 ; TITLE OF INVENTION: LIPID METABOLISM ENZYMES  
 ; FILE REFERENCE: PI-0250 USN  
 ; CURRENT APPLICATION NUMBER: US/10/398,663

; CURRENT FILING DATE: 2003-03-04  
 ; PRIOR APPLICATION NUMBER: PCT/US01/31302  
 ; PRIOR FILING DATE: 2001-10-05  
 ; PRIOR APPLICATION NUMBER: US 60/238,388  
 ; PRIOR FILING DATE: 2000-10-06  
 ; PRIOR APPLICATION NUMBER: US 60/240,616  
 ; PRIOR FILING DATE: 2000-10-13  
 ; PRIOR APPLICATION NUMBER: US 60/245,719  
 ; PRIOR FILING DATE: 2000-11-02  
 ; PRIOR APPLICATION NUMBER: US 60/247,503  
 ; PRIOR FILING DATE: 2000-11-08  
 ; PRIOR APPLICATION NUMBER: US 60/249,503  
 ; PRIOR FILING DATE: 2000-11-17  
 ; NUMBER OF SEQ ID NOS: 16  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 12  
 ; LENGTH: 1526  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; OTHER INFORMATION: Incyte ID No. US20040053281A1 7482937CB1  
 US-10-398-663-12

Query Match 4.5%; Score 46.8; DB 17; Length 1526;  
 Best Local Similarity 49.7%; Pred. No. 1.6;  
 Matches 160; Conservative 0; Mismatches 147; Indels 15; Gaps 1;

QY 318 TTGTAATGCTTTTCTTCAACAAAGATGCTTGGGTTATTCGAAGCCGTGGAACAC 377  
 Db 312 TTGCATTAATTTTGAATTTGATGATCAACGCTTACGGGATCATCATCTGTAACAATCT 371  
 QY 378 ACCTCAGTTGGAAAAATTTGAGCTGATTTTACAAAATCTATGAGAAAAATATTAAGT 437  
 Db 372 CCGTGTGTTGGTGAGTGAGTGCTTATTTATGATGTTCTCATGAAAAAATTTGAATA 431  
 QY 438 GCTGATATCAAAATATACATGATTCGGGATAGTTTGGCGCGCATCTTACAGTTTTCG 497  
 Db 432 TTCCTCTTAAAGTCACTGATTTGGCCACACGCTTGGAGACACCTGCTGGGAGGC 491  
 QY 498 GGGAAAAAGATTCAAAAGTTAAATTAAGAAATTAAGAAATTAATTCGGGCTTATCC 557  
 Db 492 TGG-----GTCAAGATACCAAGCCTTGAAGAAATTAATTCGGGCTTATCC 536  
 QY 558 TCGTGAACCGTATTTTTCATCGAGTACTGTCCGACAGACTTTCGTTAACAAGCCAGA 617  
 Db 537 AGCTGGGCAATTTTTCACAACTCCAAAGAAAGTCAAGGCTTGAACCCCTCGATGCCAA 596  
 QY 618 ATATGTTCAAGTTATCATCA 639  
 Db 597 CTTTGTGACGTTATCATCA 618

RESULT 6  
 US-10-116-802-28  
 ; Sequence 28, Application US/10116802  
 ; Publication No. US20030065157A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Amy Lasek  
 ; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER  
 ; FILE REFERENCE: PA-0045 US  
 ; CURRENT APPLICATION NUMBER: US/10/116,802  
 ; PRIOR FILING DATE: 2002-04-04  
 ; PRIOR APPLICATION NUMBER: 60/281,593  
 ; PRIOR FILING DATE: 2001-04-04  
 ; NUMBER OF SEQ ID NOS: 519  
 ; SOFTWARE: PERL Program  
 ; SEQ ID NO 28  
 ; LENGTH: 3635  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature



```
; APPLICANT: Elashoff, Michael
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5038-US
; CURRENT APPLICATION NUMBER: US/09/917,800A
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/222,040
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: US 60/222,880
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/290,029
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: US 60/290,645
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: US 60/292,336
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/295,798
; PRIOR FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/297,457
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,884
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,459
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 1740
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1549
; LENGTH: 1605
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020119462A1 NM_012597
US-09-917-800A-1549
```

Query Match 4.4%; Score 45.6; DB 9; Length 1605;

Best Local Similarity 52.1%; Pred. No. 3;

Matches 155; Conservative 0; Mismatches 134; Indels 6; Gaps 2;

```
QY 355 TATTCAGACCGTTGGAAACACACGTCAGTTGGAAAATTGTAGCTGATTTTACAAA 414
    |||||
DB 394 TATGCTATTTCGCCGCCAACACCCGTTGTGGGCCAGAGGCGCTGCTCTTCCTTA 453
    |||||
QY 415 CTACTGTGATAAATAATTAAGCTGATATCAATAATAGATTGATCGGCAATAGTTG 474
    |||||
DB 454 TGGGTGAGGAATCTATGAAGTTTCTCGAGCAAAAGTTCACTTAATTGGGTACAGCTG 513
    |||||
QY 475 GGGCGCATCTTCAGGTTTTCGGGAAAGAAAGTTCAAAAGTTAAATTAGGAAATAC 534
    |||||
DB 514 GGAGCACAGCTTCAGGATTCGAGGC-----AGCTCATGGGTGGGAAGCGCAAGATCG 568
    |||||
QY 535 AAGGAATTAATCGGGCTTGAATCTGCTGACCGTATTTCATCGGAGTGACTGTCCGAC 594
    |||||
DB 569 GAAG-AATCAAGGGCTGAGACCTCGACAGACTTATGTTTGAAGGAACCTTCCCAATGAG 627
    |||||
QY 595 AGACTTGGCTTAACAGACGAGAAATATGTTCAAGTTTATCATCATCAATCA 646
    |||||
DB 628 CGGCTTCTCCAGATGATGCCAATTGTGAGTGTATTCATTAACCTTTACCA 679
    |||||
```

#### RESULT 10

US-10-312-088-1

; Sequence 1, Application US/10312088

; Publication No. US20030219862A1

; GENERAL INFORMATION:

; APPLICANT: Agarwal, Pankaj

; APPLICANT: Cogswell, John P.

; APPLICANT: Kabutic, Karen S.

; APPLICANT: Lai, Ying-Ta

; APPLICANT: Martensen, Stelby A.

; APPLICANT: Murdock, Paul R.

; APPLICANT: Smith, Randall F.

; APPLICANT: Strum, Jay C.

; APPLICANT: Xiang, Zhaoying

```
; APPLICANT: Xie, Qing
; APPLICANT: Rizni, Safia K.
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP50029
; CURRENT APPLICATION NUMBER: US/10/312,088
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/19929
; PRIOR FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 60/213,161
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/213,156
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1383
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-312-088-1
```

Query Match 4.3%; Score 45.2; DB 17; Length 1383;

Best Local Similarity 49.4%; Pred. No. 3.5;

Matches 159; Conservative 0; Mismatches 148; Indels 15; Gaps 1;

```
QY 318 TTGTAATGCTTTGCTTCAACAAGATGCTTTGGGTTATTCCAAAGCCGTTGAAACAC 377
    |||||
DB 351 TTGCATTATTAATTAAGTTGATGTCACAGTTACGGGAATCATCATGCTTAACAATCT 410
    |||||
QY 378 ACGTCAAGTTGAAAATTTGTAGCTGATTTTACAAAACCTTGTAGAAAATATAAAGT 437
    |||||
DB 411 CCGTGTGTTGGTGCGAGGTGCTTATTTTATTAAGTCTCATGAAAAAATTTGATA 470
    |||||
QY 438 GCTGATATCAATATACGATGATCGGCAATAGTTGGCGCCCATATCTTACGTTTGC 497
    |||||
DB 471 TTCCCTCTTAAAGTCACCTGATGTCGACACCTTGGAGCACACCTGCTGGGAAAGC 530
    |||||
QY 498 GGGAAAAGAAAGTTCAAAAGTTAAATTAGGAAAATTAAGAAATTAATCGGGCTGATCC 557
    |||||
DB 531 TGG-----GTCAAGAAATACCAAGGCTTTGAAAGAAATATCTGGTTGAGCC 575
    |||||
QY 558 TGGTGAACGATATTTTATTCAGAGTGTCCGACAGACTTTGGCTAACAGACGAGA 617
    |||||
DB 576 AGCTGGGCCATTTTTCACAACTCCAAAGAAAGTCAGGCTAGACCCCTGGATGCCAA 635
    |||||
QY 618 ATATGTTCAAGTTATACATCA 639
    |||||
DB 636 CTTTGTGACGTTATCATATCA 657
    |||||
```

#### RESULT 11

US-10-403-745-2

; Sequence 2, Application US/10403745

; Publication No. US20030165975A1

; GENERAL INFORMATION:

; APPLICANT: Khodadoust, Mehran

; APPLICANT: Kapeller-Libermann, Rosana

; TITLE OF INVENTION: No. US20030165975A1 Human Lipase Proteins, Nucleic Acids Enco

; FILE REFERENCE: 10147-14

; CURRENT APPLICATION NUMBER: US/10/403,745

; CURRENT FILING DATE: 2003-03-31

; PRIOR APPLICATION NUMBER: US/09/411,132A

; PRIOR FILING DATE: 2000-09-12

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 1401

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-403-745-2

Query Match

Best Local Similarity 49.4%; Score 45.2; DB 16; Length 1401;

Matches 159; Conservative 0; Mismatches 148; Indels 15; Gaps 1;

QY 318 TTGTATGCTTTGCTTCAACAAGATGCTTTGGTTATTCGAAGCCGTTGGAACAC 377  
DB 351 TTGCATTAAATTGATTTGATGATCAACGTTTCACGGAAATGATCAATGCTGTAAACAATCT 410  
QY 378 ACCTCAGCTTGGAAAATTTGAGTATTTTACAAAACACTTGTGAAAAATATATAAGT 437  
DB 411 CGGTGTTGTTGGCGAGGTGCTTATTTTATGATGTTCTCATGAAAAAATTTGAATA 470  
QY 438 GCTGATATCAATATACGATTTATCGGGCATTTGTTGGCGCCCATTAATTCAAGTTTTC 497  
DB 471 TTCCCTCTTAAAGTCACATTTGTTGGCCACAGCTTGGAGCACACCTGGCTGGGGAAGC 530  
QY 498 GGGAAAAGAAGTTCAAAAGTTAAATTAAGGAAAAATACAGAAATTAATCGGCTGATCC 557  
DB 531 TGG-----GTCAAGGATACCAAGCCTTGGAAAGATTAAGGTTGAGCC 575  
QY 558 TGCTGACCGTATTTTCATCGAGTACTGTCCGACAGACTTTGGCTAACAGACGACAG 617  
DB 576 AGCTGGCCATTTTTCACAACACTCCAAAGAAATCAGGCTAGACCCCTCGGATGCCAA 635  
QY 618 ATATGTTCAAGTTATCATACA 639  
DB 636 CTTTGTGACGTTATTCATACA 657

## RESULT 12

US-10-038-517-1  
; Sequence 1, Application US/10038517  
; Publication No. US20020115844A1  
; GENERAL INFORMATION:  
; APPLICANT: Yu, Xuanchuan  
; APPLICANT: Turner, C. Alexander Jr.  
; TITLE OF INVENTION: No. US20020115844A1 Human Lipase and Polynucleotides Encoding  
; FILE REFERENCE: LEX-0293-USA  
; CURRENT APPLICATION NUMBER: US/10/038,517  
; PRIOR FILING DATE: 2002-01-03  
; PRIOR APPLICATION NUMBER: US 60/259,830  
; PRIOR FILING DATE: 2001-01-05  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1404  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-038-517-1

Query Match 4.3%; Score 45.2; DB 13; Length 1404;  
Best Local Similarity 49.4%; Pred. No. 3.5;  
Matches 159; Conservative 0; Mismatches 148; Indels 15; Gaps 1;

QY 318 TTGTATGCTTTGCTTCAACAAGATGCTTTGGTTATTCGAAGCCGTTGGAACAC 377  
DB 351 TTGCATTAAATTGATTTGATGATCAACGTTTCACGGAAATGATCAATGCTGTAAACAATCT 410  
QY 378 ACCTCAGCTTGGAAAATTTGAGTATTTTACAAAACACTTGTGAAAAATATATAAGT 437  
DB 411 CGGTGTTGTTGGCGAGGTGCTTATTTTATGATGTTCTCATGAAAAAATTTGAATA 470  
QY 438 GCTGATATCAATATACGATTTATCGGGCATTTGTTGGCGCCCATTAATTCAAGTTTTC 497  
DB 471 TTCCCTCTTAAAGTCACATTTGTTGGCCACAGCTTGGAGCACACCTGGCTGGGGAAGC 530  
QY 498 GGGAAAAGAAGTTCAAAAGTTAAATTAAGGAAAAATACAGAAATTAATCGGCTGATCC 557  
DB 531 TGG-----GTCAAGGATACCAAGCCTTGGAAAGATTAAGGTTGAGCC 575  
QY 558 TGCTGACCGTATTTTCATCGAGTACTGTCCGACAGACTTTGGCTAACAGACGACAG 617  
DB 576 AGCTGGCCATTTTTCACAACACTCCAAAGAAATCAGGCTAGACCCCTCGGATGCCAA 635  
QY 618 ATATGTTCAAGTTATCATACA 639

DB 636 CTTTGTGACGTTATTCATACA 657

## RESULT 13

US-10-403-745-1  
; Sequence 1, Application US/10403745  
; Publication No. US20030165975A1  
; GENERAL INFORMATION:  
; APPLICANT: Khodadoust, Mehran  
; APPLICANT: Kapeller-Liberman, Rosana  
; TITLE OF INVENTION: No. US20030165975A1 Human Lipase Proteins, Nucleic Acids Encod  
; FILE REFERENCE: 10147-14  
; CURRENT APPLICATION NUMBER: US/10/403,745  
; PRIOR FILING DATE: 2003-03-31  
; PRIOR APPLICATION NUMBER: US/09/411,132A  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 2352  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (2159)  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (2307)  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (2313)  
US-10-403-745-1

Query Match 4.3%; Score 45.2; DB 16; Length 2352;  
Best Local Similarity 49.4%; Pred. No. 4.5;  
Matches 159; Conservative 0; Mismatches 148; Indels 15; Gaps 1;

QY 318 TTGTATGCTTTGCTTCAACAAGATGCTTTGGTTATTCGAAGCCGTTGGAACAC 377  
DB 475 TTGCATTAAATTGATTTGATGATCAACGTTTCACGGAAATGATCAATGCTGTAAACAATCT 534  
QY 378 ACCTCAGCTTGGAAAATTTGAGTATTTTACAAAACACTTGTGAAAAATATATAAGT 437  
DB 535 CGGTGTTGTTGGCGAGGTGCTTATTTTATGATGTTCTCATGAAAAAATTTGAATA 594  
QY 438 GCTGATATCAATATACGATTTATCGGGCATTTGTTGGCGCCCATTAATTCAAGTTTTC 497  
DB 595 TTCCCTCTTAAAGTCACATTTGTTGGCCACAGCTTGGAGCACACCTGGCTGGGGAAGC 654  
QY 498 GGGAAAAGAAGTTCAAAAGTTAAATTAAGGAAAAATACAGAAATTAATCGGCTGATCC 557  
DB 655 TGG-----GTCAAGGATACCAAGCCTTGGAAAGATTAAGGTTGAGCC 699  
QY 558 TGCTGACCGTATTTTCATCGAGTACTGTCCGACAGACTTTGGCTAACAGACGACAG 617  
DB 700 AGCTGGCCATTTTTCACAACACTCCAAAGAAATCAGGCTAGACCCCTCGGATGCCAA 759  
QY 618 ATATGTTCAAGTTATCATACA 639  
DB 760 CTTTGTGACGTTATTCATACA 781

## RESULT 14

US-09-954-456-2217  
; Sequence 2217, Application US/09954456  
; Patent No. US20020115057A1  
; GENERAL INFORMATION:  
; APPLICANT: Young, Paul  
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc  
; FILE REFERENCE: 689290-76



```

; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2217
; LENGTH: 3549
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-2217
```

Query Match 4.3%; Score 45.2; DB 9; Length 3549;

Best Local Similarity 50.7%; Pred. No. 5.4; Matches 144; Conservative 0; Mismatches 128; Indels 12; Gaps 1;

```

QY 365 CCGTTGGAACACACGTCACGTTGGAATAATTTAGCTGATTTTACAAAATCACTAGTAG 424
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 545 CCGGGGCTACACCAAACTGGTGGACAGATGGCCGGTTTATCACTGATGAGG 604
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 425 AAAAATTAAGTCTGATATCAAAATATACGATTGATCGGCGATGTTGGCGCGCAT 484
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 605 AGGAGTTTAATCACTCCCTGACATGTCATCTCTGGGATACAGCCTTGGAGCCCATG 664
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 485 CTTAGGTTTGGCGGAAAAAGTCAAAAATTGAAAATTAAGAAATACAGAAATTA 544
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 665 CTGCTGCATTGACGGAAGTCTGACCAATAG-----AAAGTCAACAGAAATTA 712
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 545 TCGGGCTTGATCCTGCTGACCGGATTTTCATCGAGTGACTGTCCGACAGACTTTGGC 604
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 713 CTGGCCCTGATCCAGCTGACCTTAATCTTGATGACAGAAAGCCCGAGTGTCTTCTC 772
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 605 TAAACAGACGAGATATGTTCAAGTTATACATACATCAATCAT 648
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 773 CTGATGATGAGATTTTGTAGACGTCTTACACATTCACCACA 816
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

## RESULT 15

```

US-09-802-640-13
; Sequence 13, Application US/09802640
; Publication No. US20030036057A1
; GENERAL INFORMATION:
; APPLICANT: Braun, Andreas
; APPLICANT: Kiehn, Patricia
; APPLICANT: Kiehn, Patricia
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: 24736-2048
; CURRENT APPLICATION NUMBER: US/09/802,640
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 3549
; TYPE: DNA
```

```

; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (175)...(1602)
; OTHER INFORMATION: Nucleotide sequence encoding lipoprotein lipase
; OTHER INFORMATION: (LPL)
US-09-802-640-13
```

Query Match 4.3%; Score 45.2; DB 10; Length 3549;

Best Local Similarity 50.7%; Pred. No. 5.4; Matches 144; Conservative 0; Mismatches 128; Indels 12; Gaps 1;

```

QY 365 CCGTTGGAACACACGTCACGTTGGAATAATTTAGCTGATTTTACAAAATCACTAGTAG 424
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 545 CCGGGGCTACACCAAACTGGTGGACAGATGGCCGGTTTATCACTGATGAGG 604
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 425 AAAAATTAAGTCTGATATCAAAATATACGATTGATCGGCGATGTTGGCGCGCAT 484
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 605 AGGAGTTTAATCACTCCCTGACATGTCATCTCTGGGATACAGCCTTGGAGCCCATG 664
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 485 CTTAGGTTTGGCGGAAAAAGTCAAAAATTGAAAATTAAGAAATACAGAAATTA 544
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 665 CTGCTGCATTGACGGAAGTCTGACCAATAG-----AAAGTCAACAGAAATTA 712
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 545 TCGGGCTTGATCCTGCTGACCGGATTTTCATCGAGTGACTGTCCGACAGACTTTGGC 604
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 713 CTGGCCCTGATCCAGCTGACCTTAATCTTGATGACAGAAAGCCCGAGTGTCTTCTC 772
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 605 TAAACAGACGAGATATGTTCAAGTTATACATACATCAATCAT 648
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 773 CTGATGATGAGATTTTGTAGACGTCTTACACATTCACCACA 816
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

Search completed: April 29, 2005, 00:35:08  
Job time : 743 secs

**THIS PAGE LEFT BLANK**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 28, 2005, 17:13:59 ; Search time 4076 Seconds

(without alignments)  
9786.888 Million cell updates/sec

Title: US-10-688-011-1

Perfect score: 1048  
Sequence: 1 attcgtctctctgttagatga.....agtcataataaaaaaaaaa 1048

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_nuc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_g881:\*  
9: gb\_g882:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61.4	5.9	883	1	CF378395 AGENCOURT
2	60.2	5.7	343	1	AU261286 AGENCOURT
3	60.2	5.7	849	7	CF590524 AGENCOURT
4	58.2	5.6	618	7	CK149622 CamgEST00
5	57.8	5.5	517	5	BU092097 MG Apr 01
6	56.2	5.4	679	5	BM475141 BM475141
7	54.6	5.2	715	5	BM332131 BM332131
8	53.6	5.1	728	5	BM367531 BM367531
9	52.8	5.0	1086	9	CNS000YXK
10	52.4	5.0	665	7	CNS983321
11	52	5.0	363	6	CA995600
12	51.8	4.9	1101	9	CNS000DT7
13	51.4	4.9	708	5	BM355600
14	51.4	4.9	722	5	BM383883
15	51.4	4.9	758	5	BM420034
16	51.4	4.9	774	5	BM500776
17	51.4	4.9	883	5	BM482507
18	51.4	4.9	1101	9	CNS000396
19	50.4	4.8	1435	6	CD738960
20	49.6	4.7	1051	1	AA142285
21	49.6	4.7	1201	9	CNS0167M
22	49.2	4.7	866	9	CO436102
23	48	4.6	770	7	CK352674
24	48	4.6	1007	9	CNS000JOV

C	25	47.8	4.6	238	9	CNS04CWO	AL285009 Tetradon
C	26	47.6	4.5	356	7	CO722219	CO722219 Mdr30191
C	27	47.4	4.5	558	1	AV382351	AV382351 AV382351
C	28	47.4	4.5	615	7	CK134977	CK134977 RH13166.3
C	29	47.4	4.5	653	6	CD647348	CD647348 AUP 107 L
C	30	47.4	4.5	963	9	CNS00041	AL054918 Drosophila
C	31	47.2	4.5	357	9	CNS028DK	AL185852 Tetradon
C	32	47.2	4.5	426	6	CO194538	CO194538 EC82727.5
C	33	47.2	4.5	1101	9	CNS016L1	AL106896 Drosophila
C	34	47.2	4.5	237	7	CO185018	CO185018 EC29140.5
C	35	47	4.5	445	7	CF316695	CF316695 HD--06-B1
C	36	47	4.5	599	6	CA964286	CA964286 CcLX04a14
C	37	46.8	4.5	307	7	CK400031	CK400031 AGENCOURT
C	38	46.8	4.5	1362	9	AG389060	AG389060 Mus muscu
C	39	46.6	4.4	215	5	BM883483	BM883483 rc07d03.Y
C	40	46.4	4.4	717	7	CNS03847	CNS03847 Ag2_p44_F
C	41	46.4	4.4	1101	9	CNS000D1	AL055414 Drosophila
C	42	46.2	4.4	890	9	CNS00AFU	AL055222 Drosophila
C	43	45	4.4	458	2	BF710972	BF710972 MT-P-AV1-
C	44	45.8	4.4	581	5	BP257829	BP257829 BP257829
C	45	45.8	4.4	766	6	CB998818	CB998818 AGENCOURT

## ALIGNMENTS

RESULT 1  
CF378395  
LOCUS  
AGENCOURT 15349536 NICHG XGC Swb1n Xenopus tropicalis cDNA clone  
IMAGE:7004912 5', mRNA sequence.

ACCESSION  
CF378395  
VERSION  
CF378395.1  
KEYWORDS  
EST.  
SOURCE  
Xenopus tropicalis (western clawed frog)

ORGANISM  
Xenopus tropicalis  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
Xenopodinae; Xenopus; Silurana.  
1 (bases 1 to 883)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
NICHG-MGC <http://mgc.ncl.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: Rob Granger, University of Virginia

CDNA Library Preparation: Open Biosystems  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLNL4703 row: a column: 06  
High quality sequence stop: 526.  
Location/Qualifiers  
1. 883

## FEATURES

source  
/organism="Xenopus tropicalis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8364"  
/clone="IMAGE:7004912"  
/clone\_lib="whole body"  
/note="Vector: pEXpress-1; Site 1: EcoRV; Site 2: NotI;  
Bulk tissue was collected from a whole 10 month old male  
from the F6 strain. 1st strand cDNA was primed with a Not  
I - oligo(dT) primer, double-stranded cDNA was cloned into  
the Not I and EcoRV sites of pEXpress-1. Library was  
size-selected for >1.5 kb fragments for an average insert  
size of 1.92 kb. Library was normalized to Cots with a  
180-fold reduction of actin. A non-normalized version of



ORIGIN contamination by worm"

Query Match 5.7%; Score 60.2; DB 7; Length 849;  
Best Local Similarity 50.7%; Pred. No. 0.0039;  
Matches 174; Conservative 0; Mismatches 163; Indels 6; Gaps 1;

QY 355 TATTCCAAACCCCTGGAAAACACGTCACGTTGGAAAATTTGAGCTGATTTTACAAA 414  
DB 426 TACCTTATTCGCGGAGAAATACCTGATTAAGTCTAGAAAAGCTGATTTCTGAAA 485  
QY 415 CTACTTGTAGAAAATATTAAGTCTGATATCAATATAGATGATCGGACATAGTTTG 474  
DB 486 TGGGTGAGTCCTTATTCATTTTCCAAAGAGTAACATCCATTTAATTTGGGTACAGCTT 545  
QY 475 GCGCGCATATCTCAGGTTTTCGGGAAAAGAAAGTTCAAAAATTAAGAAAATAC 534  
DB 546 GAGACATGATGATCAGATTTTGCGCAGTTATATAGTGGCTTAA-----AAAGATT 599  
QY 535 AAGAAATTTATCGGCTTGTATCTGTCGACCGTATTTTATCGGAGTACGTCCGAC 594  
DB 600 GGGGAAATTCAGAGACTTGAACCCAGCTGACCATTTTGAAGAAATGTCATCTACAGAC 659  
QY 595 AGACTTTCGTTAACAAGCAGATATGTTCAAGTTATACATCATCATATTTAGGA 654  
DB 660 CGCTGTCCCAAGATGATGCTTAAGTTGTTGATGCCATTCACACATTTACTCAACAGAC 719  
QY 655 GTATATTAATAATGTTGGTTCAGTTTCTACGTGAATTATG 697  
DB 720 ATGGATTTGAGTTGGTATCAATCAGCTGTTGCCATTATG 762

RESULT 4  
CK149622 618 bp, mRNA linear EST 01-FEB-2004  
LOCUS Cullicoides sonorensis female serum-fed midgut cDNA  
DEFINITION Library Cullicoides sonorensis female serum-fed midgut cDNA  
CK149622  
ACCESSION CK149622.1 GI:41576719  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
EST.  
Cullicoides sonorensis  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Diptera; Nematocera; Chironomidae;  
Ceratopogonidae; Ceratopogoninae; Cullicoides; Monoculicoides.  
1 (bases 1 to 618)  
Campbell, C.L., Vandyke, K., Letchworth, G.J. and Wilson, W.C.  
Expressed sequence tags from Cullicoides sonorensis serum-fed female  
midguts  
unpublished (2003)  
Contact: Campbell, C.L.  
Archropod-borne Animal Diseases Research Lab  
Agricultural Research Service  
College of Agriculture, Dept. 3354, 1000 E. University Ave.,  
Laramie, WY 82071, USA  
Tel: 307 766 3626  
Fax: 307 766 3500  
Email: camcorey@uwyo.edu.  
Location/Qualifiers

FEATURES  
source  
1. .618  
/organism="Cullicoides sonorensis"  
/mol\_type="mRNA"  
/strain="AK"  
/db\_xref="taxon:179676"  
/sex="female"  
/issue\_type="midgut, serum-fed"  
/cell\_type="epithelial"  
/dev\_stage="adult"  
/clone\_id="Cullicoides sonorensis female serum-fed midgut  
cDNA library"  
/note="The Cullicoides sonorensis midgut cDNA library was  
prepared by Corey L. Campbell at the Archropod-borne  
Animal Diseases Research Lab, Laramie, WY. Marlin Larson

ORIGIN

Query Match 5.6%; Score 58.2; DB 7; Length 618;  
Best Local Similarity 50.6%; Pred. No. 0.011;  
Matches 228; Conservative 0; Mismatches 208; Indels 15; Gaps 3;

dissected midgut tissues from serum-fed adult females 2-6  
hours following a fecal bovine serum meal. Poly A+  
purified RNA ligated into pSPORT (Invitrogen). ESTs were  
amplified by PCR using M13F and M13R. The products were  
purified by ExoI digest and ethanol precipitation, then  
sequenced using T7 primer."

QY 192 ACAAGTTGATTTCTTATACATGTTTCTTCACTGGAAATATGAAACTTCGTGC 251  
DB 154 ACCAATCAAGTTGATTCATGTTTCTCAATGGCTCACTGATATGCACTAC 213  
QY 252 TATGTCGAAAGCTTTAATAGAA---AAAGATGATTTCTGTAATTCGTCGACAGAA 308  
DB 214 AGTAAAGATGCTTTATGAAAGCAGCAAGACTCAAGTCAATGTTGACTGAG 273  
QY 309 GAAAGGCTGTTGATATGCTTTGCTTCAACAAAGATGCTTGGATTTCAAAGCGT 368  
DB 274 CAAAGGTCAGTACTGTTGTC-----AAATTACTGTTGCTCATCATC 324  
QY 369 TGGAAACACAGCTCAGTGGAAATTTGTAGCTGATTTTACAAACTACTGTAGAAA 428  
DB 325 TCGAATTTGTCATGTTGGAATCAAGTCTGATTCATTTGATTTGATTCGATTA 384  
QY 429 ATATTAAGTCTGATATCAAAATPACGATTCAGGAGTATGTTGGCGCATCTTC 488  
DB 385 ACAAGATGTAACATCTTTACGTTAATTTGATGACACAGTTTGGGTCTCAAAATTC 444  
QY 489 AGGTTTTCGCGGAAAAGATTCAAAAGTTAAATTAAGAAAATPACAGAAATTTACG 548  
DB 445 TGAATTCGCGGTAAGAT---GATCGCTAGAGACACAAAGTCCATCATTTGTTG 501  
QY 549 GCTTATCTCTGTCGACCGATTTTTCATCGAGTACGTCCGACAGACTTTCGGTAC 608  
DB 502 TTGGATCTGCTCTCCCATCTTTGCTAATTAAGTGAAGTAAAGTTTGTGTCAC 561  
QY 609 AGACGCAATATGTTCAAGTTATACATACA 639  
DB 562 TGATGCCAATATGTTGAAGTTATCATTCA 592

RESULT 5  
BU092097 517 bp, mRNA linear EST 29-OCT-2003  
LOCUS gibbonus cDNA clone Mg\_AFT\_01A04 5' similar to Q02157  
DEFINITION Mg\_AFT\_01A04 M13P Mesobuthus gibbonus adult female tail Mesobuthus  
gibbosus cDNA clone Mg\_AFT\_01A04 5' similar to Q02157  
Tilacylglycerol lipase, pancreatic precu lipase (PL), mRNA  
sequence.  
BU092097  
ACCESSION BU092097.1 GI:28627351  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
EST.  
Mesobuthus gibbosus  
Mesobuthus gibbosus  
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;  
Butrida; Butchidae; Butidae; Mesobuthus.  
1 (bases 1 to 517)  
Gantenbein, B., Thomson, M., Rosie, A., Parkinson, J. and Blaxter, M.  
Gene discovery and phylogenetics of chelicerate arthropods using  
expressed sequence tags  
unpublished (2002)  
Contact: Gantenbein-Ritter B  
Institute of Cell, Animal and Population Biology  
University of Edinburgh  
West Mains Rd, Edinburgh, UK  
Email: B.Gantenbein@ed.ac.uk  
The library was prepared by Benjamin Gantenbein-Ritter and Marian  
Thomson, University of Edinburgh, from the Metasoma + Telson of an  
adult female. Sequencing was performed in Mark Blaxters lab in  
Edinburgh.

PCR primers  
 FORWARD: M13F  
 BACKWARD: PDNRlib M13R  
 Plate: 01 row: A column: 04  
 Seq primer: M13F  
 High quality sequence stop: 362.  
 Location/Qualifiers  
 1. 517

/organism="Mesobuthus gibbosus"  
 /mol\_type="mRNA"  
 /strain="Parga"  
 /db\_xref="taxon:123226"  
 /clone="Mg\_AFT\_01A04"  
 /sex="female"  
 /tissue\_type="Metasoma + Telson"  
 /dev\_stage="adult"  
 /clone\_lib="Mesobuthus gibbosus adult female tail"  
 /note="The Mesobuthus gibbosus EST library was prepared by Benjamin Gantenbein and Marian Thomson, University of Edinburgh. cDNA from the metasoma and telson of an adult female was cloned into the vector pDNR-LIB. ESTs were amplified from each clone by PCR, using primers pDNR.M13F and pDNR.M13R. The products were cleaned of excess nucleotides and phosphates, by treatment with SAP/ExoI, and then sequenced using pDNR.seq primer."

## ORIGIN

Query Match 5.5%; Score 57.8; DB 5; Length 517;  
 Best Local Similarity 53.1%; Pred. No. 0.013;  
 Matches 147; Conservative 0; Mismatches 127; Indels 3; Gaps 1;  
 QY GTAGCTGATTTTCAAAACTACTGTGAGAAATATATAAGTCTGATATCAATATACGA 456  
 Db 3 GTAGCATTTCTCTCAAGTTTGAACAGTCAATGGGAGCTGCAACATGAACTTAAT 62  
 QY TTGATCGGCGATATGTTGGCGCGCATCTTCAAGTTTGGGAAAAGAGTTCAAAAG 516  
 Db 63 GTCATGGGCGATGATTAGGATCTCATATGCACTTACGCTGATCAGGTATTAAGAA 122  
 QY TTTAAATTTAGAAATCAAGAAATTAATGAGGCTGATCCGTCGACCGTATTTTCAT 517  
 Db 123 TATTAATTTGACTTTAGGAAG--AATTAATGATGATGATGCTTAACCTTATTTTCAA 179  
 QY CGAGTGCATGTCGCGACAGACTTTCGTAACAGCAGAAATATGTCAGATTATACAT 636  
 Db 180 AATATGCCAACATATGATGATTAGATCAATCATCGATCGCATTTTGTATGCTATACAT 239  
 QY ACATCAATCATATTAGAGATATTAATATGTTGTA 673  
 Db 240 ACAGATGAAATCTATCTACTTTTGAAGTTTGGAA 276

RESULT 6  
 BM475141 679 bp mRNA linear EST 11-JUN-2004  
 LOCUS BM475141 Nori Satoh unpublished cDNA library, mature adult whole  
 DEFINITION animal Ciona intestinalis cDNA clone cima012m23 5', mRNA sequence.  
 ACCESSION BM475141  
 VERSION BM475141.1 GI:48611005  
 KEYWORDS EST.  
 SOURCE Ciona intestinalis  
 ORGANISM Ciona intestinalis  
 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
 Phlebobranchia; Clonidae; Ciona.

REFERENCE 1 (bases 1 to 679)  
 AUTHORS Satou,Y., Shin-I,T., Kohara,Y. and Satoh,N.  
 TITLE Expressed genes in Ciona intestinalis (2004)  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: Nori Satoh  
 Department of Zoology  
 Kyoto University  
 Sakyo-ku, Kyoto, Kyoto 606-8502, Japan  
 Tel: 81-75-753-4081

Fax: 81-75-705-1113  
 Email: satoh@acidian.zool.kyoto-u.ac.jp.  
 Location/Qualifiers  
 1. 679

/organism="Ciona intestinalis"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7719"  
 /clone="cima012m23"  
 /tissue\_type="whole animal"  
 /dev\_stage="mature adult"  
 /clone\_lib="Nori Satoh unpublished cDNA library, mature adult whole animal"

## ORIGIN

Query Match 5.4%; Score 56.2; DB 5; Length 679;  
 Best Local Similarity 53.9%; Pred. No. 0.031;  
 Matches 159; Conservative 0; Mismatches 133; Indels 3; Gaps 2;  
 QY 348 TTTGGGTTATTCCAAAGCCGTTGAAACACAGTCACGTTGAAAATTTGTAGCTGATT 407  
 Db 352 TGTGAATACGACACAGCGCTTCAAAACAGCGCTCTGTAGAGACGCAAGTTGTTTCT 411  
 QY 408 TCAAAACTACTTGTGAGAAAATATPAAGTCTGATATCAATATATGATGATCGGCA 467  
 Db 412 TATCAAAATGTTAATGAGAGTGTGTAACGCTGCGCTGAAAACCTTGTGCGCTT 471  
 QY 468 TAGTTTGGGCGGCGACTTCTGAGTTTGGGAAAAGAGTTCA-AAAGTAAATATAG 526  
 Db 472 CAGTTTGGTGTGACATGTAAGAGGTTTCCGCTAAGAACGTAACGACGCGGGAAG 531  
 QY 527 GAAATATACAAAGA--AATATCGGGCTTGATCTGCGACCGTATTTTCATCGAGTGA 584  
 Db 532 GCACACCGTTGACGAATACCGGTTTATGATCGGCAACCGGATTCATTCGACAA 591  
 QY 585 CTGTCCGACACACTTGTGCTGTAACAGCGCAGAAATATGTTCAAGTTATATACATA 639  
 Db 592 CTCGTCCGACACTGACCGGTTCTGACGCAAAATTCGTATGATTTATACACA 646

RESULT 7  
 BM321213 715 bp mRNA linear EST 27-MAY-2004  
 LOCUS BM321213 Yutaka Satou unpublished cDNA library, adult digestive  
 DEFINITION gland Ciona intestinalis cDNA clone cidg84if12 5', mRNA sequence.  
 ACCESSION BM321213  
 VERSION BM321213.1 GI:47743932  
 KEYWORDS EST.  
 SOURCE Ciona intestinalis  
 ORGANISM Ciona intestinalis  
 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
 Phlebobranchia; Clonidae; Ciona.

REFERENCE 1 (bases 1 to 715)  
 AUTHORS Satou,Y., Shin-I,T., Kohara,Y. and Satoh,N.  
 TITLE Expressed genes in Ciona intestinalis (2004)  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: Yutaka Satou  
 Department of Zoology  
 Kyoto University  
 Sakyo-ku, Kyoto, Kyoto 606-8502, Japan  
 Tel: 81-75-753-4095  
 Fax: 81-75-705-1113  
 Email: yutaka@acidian.zool.kyoto-u.ac.jp.  
 Location/Qualifiers  
 1. 715

/organism="Ciona intestinalis"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7719"  
 /clone="cidg84if12"  
 /tissue\_type="digestive gland"  
 /dev\_stage="adult"  
 /clone\_lib="Yutaka Satou unpublished cDNA library, adult digestive gland"

## ORIGIN

[illegible]

RESULT 8  
 BW367531  
 LOCUS 728 bp mRNA linear EST 28-MAY-2004  
 DEFINITION BW367531 Yutaka Satou unpublished cDNA library, mature adult whole animal Ciona intestinalis CDNA clone cima841k24 5', mRNA sequence.  
 ACCESSION BW367531  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Ciona intestinalis  
 Ciona intestinalis  
 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
 Phlebobranchia; Clonidae; Ciona.  
 1 (bases 1 to 728)  
 Satou, Y., Shin-I, T., Kohara, Y. and Satoh, N.  
 Expressed genes in Ciona intestinalis (2004)  
 Unpublished (2004)  
 Contact: Yutaka Satou  
 Department of Zoology  
 Kyoto University  
 Sakyo-Ku, Kyoto 606-8502, Japan  
 Tel.: 81-75-753-4095  
 Fax: 81-75-705-1113  
 Email: yutaka@acidian.zool.kyoto-u.ac.jp.

FEATURES	source
Location/Qualifiers	1..728
/organism="Ciona intestinalis"	
/mol_type="mRNA"	
/db_xref="taxon:7719"	
/clone="Cima841K24"	
/tissue_type="whole animal"	
/dev_stage="mature adult"	
/clone_lib="Yutaka Satou unpublished cDNA library, mature adult whole animal"	
ORIGIN	

	Query Match	Similarity	Score	DB	Length
Best Local	150	52.6%	51.1%	5	728
Matches	150	Conservative	0	Mismatches	120
				Indels	15
				Gaps	1
QY	354	TTATTCGAAGCGCTTGGAAACACAGCTACGCTTGAATAATTTGCTGCATTTTCAAA	4133		
DB	433	TTACGGCCAAAGCTACCGCCAAACCTCTGTCTGTAGGGGGGGAAGTTCCTCTTAATTA	4922		
QY	414	ACTACTTGTAGAAAATATTAAGTGTGATATCAATATATGATGTGTCGGCATAGTTT	4737		
DB	493	CAGGCTTAGGAGCAATCAGAGACTTTGGAAAAGATGCTCAATATTCGGSCACAGCTT	5522		

Oy GGGGGGCACTTTCAGGTTTTCGGGAAAAAGACTTCAAAAGTTAAATATAGGAATA 533  
 477 GGGGGGCACTTTCAGGTTTTCGGGAAAAAGACTTCAAAAGTTAAATATAGGAATA 533  
 Db GGGGGGCACTTTCAGGTTTTCGGGAAAAAGACTTCAAAAGTTAAATATAGGTCG----- 603  
 553 GGGGGGCACTTTCAGGTTTTCGGGAAAAAGACTTCAAAAGTTAAATATAGGTCG----- 603  
 Oy CAAGAAATATTCGGGCTGATCTCTGCTGACCCGATTTTTCATCGAGTACTGTCCGA 593  
 534 CAAGAAATATTCGGGCTGATCTCTGCTGACCCGATTTTTCATCGAGTACTGTCCGA 593  
 Db AATTACCGGGCTGATCTCTGCTGACCCGATTTTTCATCGAGAACGATCCCGTAGT 657  
 604 AATTACCGGGCTGATCTCTGCTGACCCGATTTTTCATCGAGAACGATCCCGTAGT 657  
 Oy CAGACTTTGGCTAACAGACGAGAAATATGTTCAAGTTATACATAC 638  
 594 CAGACTTTGGCTAACAGACGAGAAATATGTTCAAGTTATACATAC 638  
 Db ACGGCTGCAGCCACGAGACGCGCTGTATGTGATGCCATATACATAC 702  
 658 ACGGCTGCAGCCACGAGACGCGCTGTATGTGATGCCATATACATAC 702

RESULT 9	
CNS00YXK	1086 bp DNA linear GSS 26-JUL-1999
LOCUS	Drosophila melanogaster genome survey sequence T7 end of BAC
DEFINITION	BACN01M03 of DrosBAC library from Drosophila melanogaster (fruit fly) genomic survey sequence.
ACCESSION	AL098862
VERSION	AL098862.1 GI:5608573
KEYWORDS	GSS.
SOURCE	Drosophila melanogaster (fruit fly)
ORGANISM	Drosophila melanogaster
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
	Epiphytoidea; Drosophilidae; Drosophila.
REFERENCE	1 (bases 1 to 1086)
TITLE	Genoscope.
AUTHORS	Direct Submission
JOURNAL	Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :

COMMENT	FEATURES
<p>Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - <a href="http://www.edgp.ebi.ac.uk">http://www.edgp.ebi.ac.uk</a> - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pbeloBAC11.</p>	<p>location/Qualifiers</p> <p>1..1086</p> <p>/organism="Drosophila melanogaster"</p> <p>/mol_type="genomic DNA"</p> <p>/db_xref="taxon:7227"</p> <p>/clone_1lb="BACNO1M03"</p> <p>/clone_1lb="DrosBAC"</p> <p>/plasmid="pbeloBAC11"</p> <p>/note="end : T7"</p>

[illegible]

```

RESULT 10
LOCUS      CN9833321
DEFINITION 51953_126_038_D04 Fundulus Heteroclitus Liver Fundulus heteroclitus
            cDNA similar to Triacylglycerol 1 lipase, hepatic precursor (EC 3.1.1,
            mRNA sequence.
ACCESSION  CN9833321
VERSION     CN9833321
KEYWORDS    EST.
SOURCE      Fundulus heteroclitus (killifish)
ORGANISM    Fundulus heteroclitus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
            Cyprinodontiformes; Fundulidae; Fundulus.
REFERENCE   1 (bases 1 to 665)
            Crawford,D.L., Oleksiak,M.F., Koleil,K.J., Paschall,J., VanNye,J.,
            Roach,J.L. and Whitehead,J.A.
            Fundulus Functional Genomics: EST Database for Teleost Fish
            Unpublished (2004)
            Contact: Crawford, Douglas L.
            Marine Genomics - Crawford Lab
            Rosenstiel School of Marine and Atmospheric Science - University of
            Miami
            4600 Rickenbacker Causeway, Miami, FL 33149-1098 USA
            Tel: 305 361 4121
            Email: dcrawford@rsmas.miami.edu
            Database Web Interface
            http://genomics.rsmas.miami.edu/funnybase/super_craw3/
            Plate: 38 row: D column: 4.
            Location/Qualifiers
                source
                1..665
                /organism="Fundulus heteroclitus"
                /mol_type="mRNA"
                /db_xref="taxon:8078"
                /clone_lib="Liver"
                /clone_lib="Fundulus Heteroclitus Liver"
                /note="Organ: Liver"

ORIGIN
Query Match      5.0%; Score 52.4; DB 7; Length 665;
Best Local Similarity 51.4%; Pred. No. 0.23;
Matches 150; Conservative 0; Mismatches 136; Indels 6; Gaps 1;

QY      354 TTATTCAGAAAGCGGTGGAACACACAGTCACGTGAGAAATTTGTGATTTTACAA 413
        |||||
DB      367 TTTATCCCTGGCTGTGACAGACACCGCACTGTGGCAAGATATAGCTCATCTGCTGCA 426
        |||||
QY      414 ACTACTTGTAGAAAATATATAAAGTGTGATCAATCAATATACGATTGATCGGGCATAGTTT 473
        |||||
DB      427 GTCTCTTCAGAGAGAGTACCGGTACCGGTGAGAAAAGCTCATCTGATTGATACAGCCT 486
        |||||
QY      474 GGGCGGCGCATCTTCAGGTTTTCGGGAAAAGAGTTCAAAAGTTAAATTAGAAAAA 533
        |||||
DB      487 GGGAGGCGCATATCTGGGTTTCTGGAAGCTTCCGCAAGTTTCAGAC-----AAGAT 540
        |||||
QY      534 CAAGAAATTTATCGGGCTTGATCTGCTGGACGATATTTTCATCGAGTGCATGTCGGGA 593
        |||||
DB      541 CGGAGAGATTACCGGCTGATCCGCAAGGCGGCTGTTTGAAGGCAATGCTCTCCACGGA 600
        |||||
QY      594 CAGACTTTCGTAAACAGACGCAAGATATGTTCAAGTTATACATCAATC 645
        |||||
DB      601 CGGACTTTCCTCCGATGACGCAAGAGTTTGTGAAGCGCATCACCTTCACC 652
        |||||

RESULT 11
LOCUS      CA995600
DEFINITION 363 bp mRNA linear EST 07-JAN-2003
            r31f10.v1 Meloidogyne hapla J2 SL1 TOPO v1 Meloidogyne hapla cDNA
            5', mRNA sequence.
ACCESSION  CA995600
VERSION     CA995600.1
KEYWORDS    GI:27540471
            EST.

```

```

SOURCE      Meloidogyne hapla
ORGANISM    Meloidogyne hapla
            Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
            Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.
REFERENCE   1 (bases 1 to 363)
            McCarter,J., Clifton,S., Chiappelli,B., Page,D., Martin,J.,
            Wylie,T., Dante,M., Maira,M., Hillier,L., Kucaba,T., Theising,B.,
            Bowers,Y., Gibbons,M., Ritter,B., Bennett,J., Franklin,C.,
            Tsagarashvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,
            Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T.,
            Harvey,N., Schurk,R., Kohn,S., Shun,T., Jackson,Y., Cardenas,M.,
            McCann,R., Waterston,R. and Wilson,R.
            The Washington Univ. Nematode EST Project, 1999
            Unpublished (1999)
            Contact: McCarter JP
            The Washington Univ. Nematode EST Project, 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            The library was constructed by Claire Murphy and Dr. James McCarter
            at Washington University, St. Louis. J2 were provided by Dr.
            Valerie Williamson of the University of California at Davis
            (vwilliamson@ucdavis.edu).
            Seq primer: -40RP from Gibco
            High quality sequence stop: 351.
            Location/Qualifiers
                source
                1..363
                /organism="Meloidogyne hapla"
                /mol_type="mRNA"
                /db_xref="taxon:6305"
                /dev_stage="J2"
                /lab_host="DH10B"
                /clone_lib="Meloidogyne hapla J2 SL1 TOPO v1"
                /note="Vector: pCRIT-TOPO (Invitrogen); Site_1: EcoRI;
                Site_2: EcoRI; The library was constructed by Claire
                Murphy and Dr. James McCarter at Washington University,
                St. Louis. Oligo(dT)-SL1 PCR based library. Meloidogyne
                hapla J2 cDNA PCR products of size >400 nucleotides
                containing SL1 on the 5' end and oligo(dT) on the 3' end
                were non-directionally cloned into pCRIT-TOPO (Invitrogen)
                following the TOPO TA cloning protocol. J2 were provided
                by Dr. Valerie Williamson of University of California at
                Davis (vwilliamson@ucdavis.edu)."

ORIGIN
Query Match      5.0%; Score 52; DB 6; Length 363;
Best Local Similarity 59.5%; Pred. No. 0.27;
Matches 88; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY      901 GCATTTTAGACCGCGTTGAACCAATGACCTTATTCGCATACAGAGCGATTAACT 960
        |||||
DB      195 GCTATTATAGCAGTGGATTAATAATTAATTAATTAATAATAAAGTAGTAAAG 254
        |||||
QY      961 TAATTATAACAAAGTCAATGATACAAATAATGATATCTATGATGATTAATTAATGAAT 1020
        |||||
DB      255 TAATGAAAATAATTAATCATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 314
        |||||
QY      1021 AAACGACAGTCAATTAATAAAAAA 1048
        |||||
DB      315 AAAAAAAAAAAAAA 342
        |||||

RESULT 12
LOCUS      CNS00DT7/c
DEFINITION 1101 bp DNA linear GSS 04-JUN-1999
            Drosophila melanogaster genome survey sequence TE13 end of BAC #
            BACR28J21 of RPC1-98 library from Drosophila melanogaster (fruit
            fly) genomic survey sequence.
ACCESSION  AL075293
VERSION     AL075293.1
KEYWORDS    GI:4948467
            GSS.

```



SOURCE	Drosophila melanogaster (fruit fly)
ORGANISM	Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Peiryogeta; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydrioidae; Drosophilidae; Drosophila.
REFERENCE	1 (bases 1 to 1101) Genoscope. Direct Submission Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : sequefgenoscope.cns.fr - Web : www.genoscope.cns.fr) Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoko Osoegawa and Aaron Mamoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RCFI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
AUTHORS	
TITLE	
JOURNAL	
COMMENT	
FEATURES	Location/Qualifiers source 1..1101 /organism="Drosophila melanogaster" /mol_type="genomic DNA" /db_xref="taxon:7227" /clone="BACR28U21" /clone_1lb="RCFI-98" /note="end : TET3"
ORIGIN	
Query Match	4.9%; Score 51.8; DB 9; Length 1101;
Best Local Similarity	30.8%; Pred. No. 0.33;
Match 125; Conservative	73; Mismatches 208; Indels 0; Gaps 0;
OY	33 TAGAATGTCCTGAATAGACGATGTCCGGATTGACTTTTAAGAAGAATAT 92
DB	1101 TAAAMATAATMTTATATATATATATATTAATAAAMATAMATAATAATATTTAT 1042
OY	93 AGATTTCTATGTTATCTCAAGGATTAACGAGATGTTATTTCTTAAGAAAACCTT 152
DB	1041 TTATTTATTAATMTATATATATATATATATATATATATATATATATATATTT 982
OY	153 AACGAATTAACGATCGTTTACAAGCTCAACAATCAACAAGTGATTTCTTATACA 212
DB	981 WMTTTTTTTTTTTTTTTTTTTTATATATATATATATATTTTTTTTTTTTTTTTT 922
OY	213 TGTTTCTTCACTGGGAATAATGAAGAACCTGTCATATGTCGAAGCTTAAATGA 272
DB	921 TWTTTTWTATMAATMTATMTATMAAATTTTTTTTTTWTATATATATATTTT 862
OY	273 AAAAGATGATTTCTTGTATATTTCCGTCAGCATGAAGAAGGTCCTGTATGCTTTGC 332
DB	861 ATTMTTTTWTTTTTTTTATTTTTTTTTTTTKGGKGGGGGGGGGGGGGGGGGB 802
OY	333 TTCACAAAGATGCTTTGGGTATTTCCAAGCCGTGGAACAACAGTCAGTTGAAA 392
DB	801 BSBBVBNNVVNTTTTTTTTTNNNNNNNNRRRRRRRRRRRGGRGCGNNNNNNRRA 742
OY	393 ATTTGTACGATTTTACAACACTCTGTGAAGAAAAATATAAGG 438
DB	741 AAGAGAGATGTTAATARRAAGTAGAAGAADPAARARRRRRRARG 696
RESULT 13	
LOCUS	BW365600 708 bp linear EST 28-MAY-2004
DEFINITION	BW365600 Yutaka Satou unpublished cDNA library, mature adult whole

ACCESSION		animal Ciona intestinalis cDNA clone cima836c06 5', mRNA sequence.
VERSION	BW365600.1	GI:47781428
KEYWORDS	EST.	
SOURCE	Ciona intestinalis	
ORGANISM	Ciona intestinalis	
REFERENCE	Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;	
AUTHORS	Phlebobranchia; Cionidae; Ciona.	
TITLE	1 (bases 1 to 708)	
JOURNAL	Satou,Y., Shin-I,T., Kohara,Y. and Satoh,N.	
COMMENT	Expressed genes in Ciona intestinalis (2004)	
	Unpublished (2004)	
	Contact: Yutaka Satou	
	Department of Zoology	
	Kyoto University	
	Sakyo-ku, Kyoto, Kyoto 606-8502, Japan	
	Tel.: 81-75-753-4095	
	Fax: 81-75-705-1113	
	Email: yutaka@ascidian.zool.kyoto-u.ac.jp.	
FEATURES	Location/Qualifiers	
source	1..708	
	/organism="Ciona intestinalis"	
	/mol_type="mRNA"	
	/db_xref="taxon:7719"	
	/clone="cima836c06"	
	/issue_type="whole animal"	
	/dev_stage="mature adult"	
	/clone_id="Yutaka Satou unpublished cDNA library, mature	
	adult whole animal"	
ORIGIN		
Query Match	4.9%; Score 51.4; DB 5; Length 708;	
Best Local Similarity	52.3%; Pred. No. 0.39;	
Matches 149; Conservative	0; Mismatches 121; Indels 15; Gaps 1;	
OY	354 TTATTCAGAACCGCTTGAAAACACAGCATCGTTGGAAAAATTGCTACTGATTTTACAA	413
DB	429 TTACGGCCCAACCTACCCGCCAACCCTGTGTGAAGGGCGGAGATTCCTCTTAATTAA	488
OY	414 ACTACTGTGATAAAATATAAAGTCGATVTCAAATATACGATTGATCGGGCATAGTTT	473
DB	489 CAGCTTGAAGAGCAATCAGAGCCCTTGAAAGAAATGCATATCATCGCACACACTT	548
OY	474 GGGCGCGCATCTTCAGGTTTTGGCGGAAAAAGATTCAAAGTTAAATTAGAAAAATA	533
DB	549 GGGCGCACACGTCCTGCTATGCTGTGTAAGAATTAAAGTTAGTGC-----	599
OY	534 CAAGAAATATATCGGCGCTTGATCTGCTGCAGCCGATATTTTCATGGAGTACTGCCGA	593
DB	600 -----AATTACCGCGCTCGATCCAGCTGAGCCGTTTTATCAAGSAAGATCCCGTAGT	653
OY	594 CAGACTTGGGTACAGACGCAAGATATGTTCAGAGTTATACATATC	638
DB	654 ACGGCTGCAACCAACAGACGCGCTGTATGTGATGCCATACATAC	698
RESULT 14		
BW383883/c	722 bp	mRNA linear EST 28-MAY-2004
LOCUS		
DEFINITION	BW383883 Yutaka Satou unpublished cDNA library, adult digestive	
	gland Ciona intestinalis cDNA clone cidg834k21 3', mRNA sequence.	
ACCESSION	BW383883	
VERSION	BW383883.1	GI:47799711
KEYWORDS	EST.	
SOURCE	Ciona intestinalis	
ORGANISM	Ciona intestinalis	
	Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;	
	Phlebobranchia; Cionidae; Ciona.	
REFERENCE	1 (bases 1 to 722)	
AUTHORS	Satou,Y., Shin-I,T., Kohara,Y. and Satoh,N.	
TITLE	Expressed genes in Ciona intestinalis (2004)	
JOURNAL	Unpublished (2004)	
COMMENT	Contact: Yutaka Satou	



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 28, 2005, 17:08:05 ; Search time 4887 Seconds

(Without alignments)  
10391.051 Million cell updates/sec

Title: US-10-688-011-1

Perfect score: 1048  
Sequence: 1 atttgccttcgttcgatgta.....agtcataataaaaaaaaaa 1048

Scoring table:

IDENTITY-NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBank1:\*  
1: gb\_ba:\*  
2: gb\_hgc:\*  
3: gb\_in:\*  
4: gb\_cm:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sv:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1048	100.0	1048	AF174527	AF174527 Polistes
2	1048	100.0	1048	BD223803	BD223803 Cloning a
3	1048	100.0	1048	AR206946	AR206946 Sequence
4	1048	100.0	1048	AR431328	AR431328 Sequence
5	818.4	78.1	1171	AY566645	AY566645 Polistes
6	782.4	74.7	948	AY566646	AY566646 Polistes
7	779.2	74.4	948	AY566647	AY566647 Polistes
8	777.6	74.2	948	AY566649	AY566649 Polistes
9	441	42.1	1050	AR162936	AR162936 Sequence
10	441	42.1	1050	AR162937	AR162937 Sequence
11	441	42.1	1050	AR162938	AR162938 Sequence
12	441	42.1	1050	AR162939	AR162939 Sequence
13	441	42.1	1050	AR162940	AR162940 Sequence
14	429.4	41.0	1324	VESAPVIR	VESAPVIR Vespa
15	426.2	40.7	1341	AR162937	AR162937 Sequence
16	426.2	40.7	1341	AR162938	AR162938 Sequence
17	426.2	40.7	1341	AR162939	AR162939 Sequence
18	426.2	40.7	1341	AR162940	AR162940 Sequence
19	426.2	40.7	1341	AR206927	AR206927 Sequence

20	425.2	40.6	1143	3	DMDOLMT	X66869 D. maculata
21	87.8	8.4	1189	3	AY684998	AY684998 Solenopsis
22	59	5.6	1141	6	AX083744	AX083744 Sequence
23	51.2	4.9	3213	4	MVILPOLIP	AJ223493 Mustela v
24	50.2	4.8	12353	1	AE007710	AE007710 Clostridi
25	49.8	4.8	1511	4	FCU42725	U42725 Felis catu
26	49.2	4.7	14536	3	AF467260	AF467260 Oestrinia
27	49	4.7	1301	6	CQ578568	CQ578568 Sequence
28	49	4.7	1338	3	AY094909	AY094909 Drosophila
29	49	4.7	4016	6	CQ578567	CQ578567 Sequence
30	49	4.7	51050	3	AC004340	AC004340 Drosophila
31	49	4.7	85539	2	AC019877	AC019877 Drosophila
32	49	4.7	175867	3	AC007976	AC007976 Drosophila
33	49	4.7	184650	3	AC092186	AC092186 Drosophila
34	49	4.7	303641	3	AE003583	AE003583 Drosophila
35	48.6	4.6	349980	6	AX344560	AX344560 Sequence
36	48.2	4.6	1394	3	AF489470	AF489470 Ceratobae
37	48.2	4.6	1733	5	BC053243	BC053243 Dario rex
38	48.2	4.6	105682	3	AC116957_3	Continuation (4 of
39	48	4.6	1595	4	AY559452	AY559452 Sus scrofa
40	47.6	4.5	14535	4	AF442957	AF442957 Oestrinia
41	47.6	4.5	85467	9	AL133457	AL133457 Human DNA
42	47.6	4.5	146706	2	CR450735	CR450735 Dario rex
43	47.6	4.5	184610	2	AC009924	AC009924 Homo sapi
44	47.4	4.5	12184	3	AY372120	AY372120 Plasmodiu
45	47.4	4.5	250029	3	AE014839	AE014839 Plasmodiu

## ALIGNMENTS

RESULT 1  
AF174527  
LOCUS AF174527 1048 bp mRNA linear INV 01-SEP-1999  
DEFINITION Polistes annularis phospholipase A1 mRNA, complete cds.  
ACCESSION AF174527  
VERSION AF174527.1 GI:5815248  
KEYWORDS  
SOURCE  
ORGANISM Polistes annularis  
Polistes annularis  
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;  
Vespoidea; Vespidae; Polistinae; Polistes.  
REFERENCE  
1 (bases 1 to 1048)  
AUTHORS King, T.P. and Lu, G.  
TITLE Direct Submission  
JOURNAL Submitted (03-AUG-1999) Rockefeller University, 1230 York Ave., New York, NY 10021, USA

## FEATURES

source location/Qualifiers  
1..1048  
/organism="Polistes annularis"  
/mol\_type="mRNA"  
/db\_xref="taxon:27505"  
58..963  
/note="venom allergen"  
/codon\_start=1  
/product="phospholipase A1"  
/protein\_id="AAD52615.1"  
/db\_xref="GI:5815249"  
/translation="MSPTGKNSKQIVFVYSRDKRGGIILKKETLTNYDLPTKSTIS  
KQVRLIRFLSTGNNEFNVMASKLIEQDPLVIVSVPKAKACNAPATKRALGYSK  
AVGNTRVGRFVADFTKLIVERYKVLISNRLIGHSLGHTGPFACKVQKILGKYK  
EIIQDPAGVPHRSDCPRLCVTDAEVQVHTSIILGVYVNGSVDFVYVYGNQKP  
GNBPSCHTKAVKYLTECIKHECCILGPMKKYFSTPPIISQCGDTCVGLNKKSS  
YPARGAFVAPVEANAPYCHNEGIKL"

## ORIGIN

Query Match 100.0%; Score 1048; DB 3; Length 1048;  
Best Local Similarity 100.0%; Pred. No. 9.1e-195;  
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 ATTGCTTCTGTGATGATTCGACGACATTTAGAAATGTTACCTTAATGAGCGATG 60  
|||||

```

Db      1 ATTGCTCTCTGTTAGATGATTCGACGACATTTAGAAATGTTACTTGATAGAGGCATG 60
QY      61 TCTCCGAGATTGACTTTTAATGAGAAAGATATGATTTCTAGCTTACCAAGGATAG 120
Db      61 TCTCCGAGATTGACTTTTAATGAGAAAGATATGATTTCTAGCTTACCAAGGATAG 120
QY      121 CGAGATGATTAATTTCTTAAGAAAGAACTTTAACAATTTAGATCTGTTTCAAAAGTCT 180
Db      121 CGAGATGATTAATTTCTTAAGAAAGAACTTTAACAATTTAGATCTGTTTCAAAAGTCT 180
QY      181 ACAATATCAAAACAGTTGATTTCTTAATACATGTTTCTTCAACTGGGAATATGAA 240
Db      181 ACAATATCAAAACAGTTGATTTCTTAATACATGTTTCTTCAACTGGGAATATGAA 240
QY      241 AACTTGCTGCTATGTCGAAAGCTTAAATAGAAAAGATTTCTTGTAAATTCGGTTC 300
Db      241 AACTTGCTGCTATGTCGAAAGCTTAAATAGAAAAGATTTCTTGTAAATTCGGTTC 300
QY      301 GACTGGAAGAGGGTCTGTAATGCTTTTGTCTTCAACAAGAGATCTTTGGGTTATTC 360
Db      301 GACTGGAAGAGGGTCTGTAATGCTTTTGTCTTCAACAAGAGATCTTTGGGTTATTC 360
QY      361 AAAGCCGTTGGAACAACAGTCACGTTGGAATTTTGTAGCTGATTTTCAAAACTACTT 420
Db      361 AAAGCCGTTGGAACAACAGTCACGTTGGAATTTTGTAGCTGATTTTCAAAACTACTT 420
QY      421 GTAGAAAAATATTAAGTGTGATATCAATATATACATGATGCGGCGATGTTGGGCGG 480
Db      421 GTAGAAAAATATTAAGTGTGATATCAATATATACATGATGCGGCGATGTTGGGCGG 480
QY      481 CATACTTCAGGTTTTCGGGAAAAAGAAAGTTCAAAAGTTAAATTTAGAAAAATACAGAA 540
Db      481 CATACTTCAGGTTTTCGGGAAAAAGAAAGTTCAAAAGTTAAATTTAGAAAAATACAGAA 540
QY      541 ATTATCGGGCTGATCTCTGTCGACCGTATTTTCACTGAGATGCTGTCGACAGACTT 600
Db      541 ATTATCGGGCTGATCTCTGTCGACCGTATTTTCACTGAGATGCTGTCGACAGACTT 600
QY      541 ATTATCGGGCTGATCTCTGTCGACCGTATTTTCACTGAGATGCTGTCGACAGACTT 600
Db      541 ATTATCGGGCTGATCTCTGTCGACCGTATTTTCACTGAGATGCTGTCGACAGACTT 600
QY      601 TCGGTACAGACGACAGATATGTTCAAGTTATACATACATCATATTTAGAGATAT 660
Db      601 TCGGTACAGACGACAGATATGTTCAAGTTATACATACATCATATTTAGAGATAT 660
QY      661 TATATGTTGTAGACGTTGATTTCTACGTGAATTTATGAAAAATCAACCTGGTTCAT 720
Db      661 TATATGTTGTAGACGTTGATTTCTACGTGAATTTATGAAAAATCAACCTGGTTCAT 720
QY      721 GAACCATCTCTCTCTATACGAAAGCCGTGAATATCTGATGATGCTAATAACATGAA 780
Db      721 GAACCATCTCTCTCTATACGAAAGCCGTGAATATCTGATGATGCTAATAACATGAA 780
QY      781 TGTGTTTAAATTTGAAACACATGGAAGAAATATTTGAGACTCCAAAACCAATTTCCGAG 840
Db      781 TGTGTTTAAATTTGAAACACATGGAAGAAATATTTGAGACTCCAAAACCAATTTCCGAG 840
QY      841 TCGAGAGAGACACCTGTGTTGCGTTGATTTGAATGCAAAAAGTTATCTCTGAGAGC 900
Db      841 TCGAGAGAGACACCTGTGTTGCGTTGATTTGAATGCAAAAAGTTATCTCTGAGAGC 900
QY      901 GCATTTTATGACCCGTTGAGCAATGACCTTATTTGCAATAGAGAGGATTAATCTT 960
Db      901 GCATTTTATGACCCGTTGAGCAATGACCTTATTTGCAATAGAGAGGATTAATCTT 960
QY      961 TAAATATAAACAAGTCAATGATACAAAAATGATCTATGATGAATATTAATGAAT 1020
Db      961 TAAATATAAACAAGTCAATGATACAAAAATGATCTATGATGAATATTAATGAAT 1020
QY      1021 AAACGACGTCAAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1048
Db      1021 AAACGACGTCAAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1048

```

RESULT 2  
BD223803

```

LOCUS      BD223803              1048 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION Cloning and recombinant production of polistinae toxin enzymes
            (phospholipase, hyaluronidase, etc.) and immunological therapy
            based thereon.
ACCESSION  BD223803
VERSION    BD223803.1 GI:33033573
KEYWORDS   JP 2002525107-A/1.
SOURCE     Polistes annularis
ORGANISM   Polistes annularis
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Peerygota;
            Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
            Vespoidea; Vespidae; Polistinae; Polistes.
            1 (bases 1 to 1048)
REFERENCE  King, T. P.
            Cloning and recombinant production of polistinae toxin enzymes
            (phospholipase, hyaluronidase, etc.) and immunological therapy
            based thereon
            Patent: JP 2002525107-A 1 13-AUG-2002;
            THE ROCKEFELLER UNIVERSITY
COMMENT    OS Polistes annularis
            PN JP 2002525107-A/1
            PD 13-AUG-2002
            PF 01-OCT-1999 JP 2000572343
            PR 01-OCT-1998 US 09/166205
            PI TE PAIO KING
            PC C12N15/09,A61K38/46,A61P31/12,A61P31/18,A61P37/06,
            PC C07K19/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/16,C12N9/
            PC 26,C12N15/00,
            PC C12N5/00,A61K37/54
            CC Cloning and recombinant production of polistinae toxin enzymes
            CC (phospholipase, hyaluronidase, etc.) and
            CC immunological therapy
            CC based
            CC thesoron
            CC key
            FT source
            FT 1. .1048
            FT /organism='Polistes annularis'.
            FT /organism='Polistes annularis'
            FT /mol_type='genomic DNA'
            FT /db_xref='taxon:27505'

FEATURES
     source
     location/Qualifiers
     1. .1048
     /organism='Polistes annularis'
     /mol_type='genomic DNA'
     /db_xref='taxon:27505'

ORIGIN
Query Match 100.0%; Score 1048; DB 6; Length 1048;
Best Local Similarity 100.0%; Pred. No. 9.1e-195;
Matches 1048; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATTGCTCTCTGTTAGATGATTCGACGACATTTAGAAATGTTACTTGATAGAGGCATG 60
Db      1 ATTGCTCTCTGTTAGATGATTCGACGACATTTAGAAATGTTACTTGATAGAGGCATG 60
QY      61 TCTCCGAGATTGACTTTTAATGAGAAAGATATGATTTCTAGCTTACCAAGGATAG 120
Db      61 TCTCCGAGATTGACTTTTAATGAGAAAGATATGATTTCTAGCTTACCAAGGATAG 120
QY      121 CGAGATGATTAATTTCTTAAGAAAGAACTTTAACAATTTAGATCTGTTTCAAAAGTCT 180
Db      121 CGAGATGATTAATTTCTTAAGAAAGAACTTTAACAATTTAGATCTGTTTCAAAAGTCT 180
QY      181 ACAATATCAAAACAGTTGATTTCTTAATACATGTTTCTTCAACTGGGAATATGAA 240
Db      181 ACAATATCAAAACAGTTGATTTCTTAATACATGTTTCTTCAACTGGGAATATGAA 240
QY      241 AACTTGCTGCTATGTCGAAAGCTTAAATAGAAAAGATTTCTTGTAAATTCGGTTC 300
Db      241 AACTTGCTGCTATGTCGAAAGCTTAAATAGAAAAGATTTCTTGTAAATTCGGTTC 300
QY      301 GACTGGAAGAGGGTCTGTAATGCTTTTGTCTTCAACAAGAGATCTTTGGGTTATTC 360
Db      301 GACTGGAAGAGGGTCTGTAATGCTTTTGTCTTCAACAAGAGATCTTTGGGTTATTC 360

```

	Matches	1048:	Conservative	0:	Mismatches	0:	Indels	0:	Gaps	0:
Qy	1	ATTGCTTCTTGATAGATGATTCGACGACATTTAGAAATGCTACCTTGAAATAGAGCATG	60							
Db	1	ATTTCCTTCTTGATAGATTCGACGACATTTAGAAATGCTACCTTGAAATAGAGCATG	60							
Qy	61	TCTCCGATGTGACTTTTAATGAGAAAGATATAGATTTCTATGTTTACTCAAGGATTAAG	120							
Db	61	TCTCCGATGTGACTTTTAATGAGAAAGATATAGATTTCTATGTTTACTCAAGGATTAAG	120							
Qy	121	CGAATGATTAATCTTAAGAAAGAACTTAAAGAAATACGATCTGTTTACAAAGCT	180							
Db	121	CGAATGATTAATCTTAAGAAAGAACTTAAAGAAATACGATCTGTTTACAAAGCT	180							
Qy	181	ACAATATCAAAACAAGTTGATTTCTATACAGGTGCTCTTCAACTGGGAATATGAA	240							
Db	181	ACAATATCAAAACAAGTTGATTTCTATACAGGTGCTCTTCAACTGGGAATATGAA	240							
Qy	241	AACTTCGTTGCTATGTGAAAAGCTTAAATAGAAAAGTGAATTTTCTGTATTTCCGCTC	300							
Db	241	AACTTCGTTGCTATGTGAAAAGCTTAAATAGAAAAGTGAATTTTCTGTATTTCCGCTC	300							
Qy	301	GACTGGAAAGAGGGGCTGTATATGCTTTTGCTCAACAAAGATGCTTGGGTTATCC	360							
Db	301	GACTGGAAAGAGGGGCTGTATATGCTTTTGCTCAACAAAGATGCTTGGGTTATTC	360							
Qy	361	AAAGCCGTGGAAACAACGTCAGGTTGAAAATTTGTAGCTGATTTTACAAACTACTT	420							
Db	361	AAAGCCGTGGAAACAACGTCAGGTTGAAAATTTGTAGCTGATTTTACAAACTACTT	420							
Qy	421	GTAGAAAAATATTAAGTCTGATATCAATATACGATTTGATCGGCAATAGTTTGGGCGCG	480							
Db	421	GTAGAAAAATATTAAGTCTGATATCAATATACGATTTGATCGGCAATAGTTTGGGCGCG	480							
Qy	481	CATACCTCAGGTTTGGCGGAAAAAGAGTTCAAAAGTTAAATAGGAAAAATACAGGAA	540							
Db	481	CATACCTCAGGTTTGGCGGAAAAAGAGTTCAAAAGTTAAATAGGAAAAATACAGGAA	540							
Qy	541	ATTATCGGGCTGATTCCTGCTGACACCGTATTTTCAATCGAGTGAATGCTCCGACAGACTT	600							
Db	541	ATTATCGGGCTGATTCCTGCTGACACCGTATTTTCAATCGAGTGAATGCTCCGACAGACTT	600							
Qy	601	TGCGTAACAGACGACGAATATGTTCAAGTTATACATCATCATATTAAGAGTATAT	660							
Db	601	TGCGTAACAGACGACGAATATGTTCAAGTTATACATCATCATATTAAGAGTATAT	660							
Qy	661	TATATATGTTGATACGCTGATTTCTACGTGAATTAAGAAAAATCAACCTGTTGCAAT	720							
Db	661	TATATATGTTGATACGCTGATTTCTACGTGAATTAAGAAAAATCAACCTGTTGCAAT	720							
Qy	721	GAAACATCTCTCTCATACGAAAGCCGTGAATATCTGACTGATGATTAACATGAA	780							
Db	721	GAAACATCTCTCTCATACGAAAGCCGTGAATATCTGACTGATGATTAACATGAA	780							
Qy	781	TGTTGTTTAATGGAACAACATGGAAGAAATATTTGACACTCCGAAAACCAATTTCCAG	840							
Db	781	TGTTGTTTAATGGAACAACATGGAAGAAATATTTGACACTCCGAAAACCAATTTCCAG	840							
Qy	841	TGCAAGAGACACCTGTGTTGGCTGTTGATGTAATGCAAAAAGTATCTCTGTAGAGGC	900							
Db	841	TGCAAGAGAGCACCTGTGTTGGCTGTTGATGTAATGCAAAAAGTATCTCTGTAGAGGC	900							
Qy	901	GCAATTTATGACACCGGTTGAAGCAATATGCACTTAATGCAATGCAAGGGGATTAACCTT	960							
Db	901	GCAATTTATGACACCGGTTGAAGCAATATGCACTTAATGCAATGCAAGGGGATTAACCTT	960							
Qy	961	TAAATTAATAACAAAGTCAATGTACACAAAATGTATCTATGATGAAATATTAATGAAT	1020							
Db	961	TAAATTAATAACAAAGTCAATGTACACAAAATGTATCTATGATGAAATATTAATGAAT	1020							
Qy	1021	AAACGAACAGTCAATTAATAAAAAAAAAA	1048							
Db	1021	AAACGAACAGTCAATTAATAAAAAAAAAA	1048							

[illegible]

Query Match	78.1%	Score 818.4	DB 3	Length 1171
Db	661	TATATGTGGTACGGTTGATTTCTACGTGATTTATCGAAAAATCAACTGGTTGCAAT	720	
Qy	721	GAACCATCTGCTCTCATACGAAAGCCGTGAAATATTTGACTGATGCAATPAAACATGAA	780	
Db	721	GAACCATCTGCTCTCATACGAAAGCCGTGAAATATTTGACTGATGCAATPAAACATGAA	780	
Qy	781	TGTTGTTTAATTGGAACACCATGGAAACAATATTTTGACATCCAAAACAATTTCCAG	840	
Db	781	TGTTGTTTAATTGGAACACCATGGAAACAATATTTTGACATCCAAAACAATTTCCAG	840	
Qy	841	TGCAGAGAGACACCTGTGTTTGGCTGGATTTGAATGCAAAAAAGTTATCTGCTAGAGGC	900	
Db	841	TGCAGAGAGACACCTGTGTTTGGCTGGATTTGAATGCAAAAAAGTTATCTGCTAGAGGC	900	
Qy	901	GCATTTTATGACCCGGTTGAAGCAAAAGCACTTATTTGCCATTAACGAGGGGATTTAACTT	960	
Db	901	GCATTTTATGACCCGGTTGAAGCAAAAGCACTTATTTGCCATTAACGAGGGGATTTAACTT	960	
Qy	961	TAATTATPAAACAAGTCATATGTCACAAAATGTATCTATTGATGAAATTTAAATGAAT	1020	
Db	961	TAATTATPAAACAAGTCATATGTCACAAAATGTATCTATTGATGAAATTTAAATGAAT	1020	
Qy	1021	AAACGAAACGTCGAATTAATPAAAAA	1048	
Db	1021	AAACGAAACGTCGAATTAATPAAAAA	1048	
RESULT 5				
LOCUS	AY566645	1171 bp	mRNA	linear
DEFINITION	Polistes dominulus venom phospholipase A1 1 precursor mRNA,			
ACCESSION	AY566645			
VERSION	AY566645.1	GI:45510886		
KEYWORDS				
ORGANISM	Polistes dominulus (European paper wasp)			
REFERENCE	Polistes dominulus			
AUTHORS	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;			
JOURNAL	Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;			
	Vespoidea; Vespidae; Polistinae; Polistes.			
	1 (bases 1 to 1171)			
	Moawad,T.I.S. and Hoffman,D.R.			
	Direct Submission			
	Submitted (05-MAR-2004) Pathology and Laboratory Medicine			
	Department, Brody School of Medicine, East Carolina University, 600			
	Moye Blvd., Greenville, NC 27858, USA			
FEATURES	Location/Qualifiers			
source	1..1171			
	/organism="Polistes dominulus"			
	/mol_type="mRNA"			
	/db_xref="taxon:34728"			
CDS	55..1068			
	/note="allergen Pol d 1.01"			
	/codon_start=1			
	/product="venom phospholipase A1 1 precursor"			
	/protein_id="AA567041.1"			
	/translation="MNPKYSILPICEVKVLNDCYADDLTLLNGTLDRGITDCTFN			
	EXKILIEHVSRRDKNGLILKEELIKNYDIFQKQISHQIILHGFISTGNENPFAM			
	AKKILIEDNPLVSVWKGACNAFASNDVLGVSQAVGNTBVGKVDLPFTLLVEQ			
	YKPKMSNIRLIGHSLGHTSGFAGKEVORIKTKYKEIIGLDAGSPFLTKCPNRLC			
	EPDAVQALHTSRAITLIGVYNNGSNDPVYNNKSGSCSPSHTKAVYLYECLIKR			
	ECLLIGTPKMSYSTRPKFISQCRDTCVGLNAQSPAKGSFYVPDKDAPIYCHNKG			
	IKI"			
	55..117			
	118..1065			
	/note="encodes venom phospholipase A1 1 proenzyme"			
	160..1065			
	/product="venom phospholipase A1 1"			
ORIGIN				

Best Local Similarity 86.9%; Pred. No. 6,4e-150;  
Matches 911; Conservative 0; Mismatches 136; Indels 1; Gaps 1;

```

QY 1 ATTGCTCTTGTAGATTCGACGACATTTGAAGTGTACCTTGAATGAGCGATG 60
DB 106 AATGTTACCGCGGTGATGATTTGACACCCCTGGAATGGTACCTTGACAGAGGCATC 165
QY 61 TCTCCGATTTGATCTTTAATGAGAAAGATATGATTTCTATGTTTACTGAGGATTAAG 120
DB 166 ACTCCGATTTGATCTTTAATGAGAAAGATATGAGTACCGTTTACTGAGGATTAAG 225
QY 121 CGAGATGATATTTCTTAAGAAAGAACTTAAAGATTAACGATTCGTTTACAAATCT 180
DB 226 CGAAATGATATTTCTTAAGAAAGAAATTTTAAGATTAACGATTCGTTTCAAAATCT 285
QY 181 ACAATATCAAAACAGTTGATTTCTTAATCATGTTTCTTCACTGGGAATATGA 240
DB 286 CAATATCATCATCAATTTGCAATTTCTTAATCATGTTTCTTCACTGGGAATATGA 345
QY 241 AACTTCTTGTATGTTGAAAGCTTTAATGAAAAAGATTTTCTTGTATTTTGGTTC 300
DB 346 AATTTTCATCATGCGGAAAGCTTTGATGAAATGATATATTTCTTGTATTTTGGTTC 405
QY 301 GACTGAAAGAGGCTTGTATGCTTTTGTCTTCAAGAAAGATGCTTGGGTATTTCC 360
DB 406 GACTGAAAGAGGCTTGTATGCTTTTGTCTTCAAGAAAGATGCTTGGGTATTTCC 465
QY 361 AAAGCCGTTGAAACACACGTCACGTTGAAATTTGTAGCTGATTTTACAAACTACT 420
DB 466 CAAGCCGTTGAAACACACGTCACGTTGAAATTTGTAGCTGATTTTACAAACTACT 525
QY 421 GTTGAAGAAATTAAGTCTGATTCATTAATGATGATGATCGGCACTAGTTGGCGCG 480
DB 526 GTTGAAGAAATTAAGTCTGATTCATTAATGATGATGATCGGCACTAGTTGGCGCG 585
QY 481 CATACTTCAGGTTTGGCGGAAAGAACTTCAAAAGTTAAATTAAGAAATTAAGAA 540
DB 586 CATACTTCAGGTTTGGCGGAAAGAACTTCAAAAGTTAAATTAAGAAATTAAGAA 645
QY 541 ATTATCGGCGCTTGAATCTGCTGAGACCGTATTTTCTATGAGATGCTGCGGACACT 600
DB 646 ATTATCGGCGCTTGAATCTGCTGAGACCGTATTTTCTATGAGATGCTGCGGACACT 705
QY 601 TGGGTAAACAGACGCAAGATATGTTCAAGTATATCATCATCATATTAAGATATAT 660
DB 706 TGGGTAAACAGACGCAAGATATGTTCAAGTATATCATCATCATATTAAGATATAT 765
QY 661 TATATGTTGATGAGCTTGAATTTCTACGTAATTAAGAAATTAAGAAATTAAGAA 720
DB 766 TATATGTTGATGAGCTTGAATTTCTACGTAATTAAGAAATTAAGAAATTAAGAA 825
QY 721 GAAACATCTCTGCTCTCATACGAAAGCCGTGAAATATCTGACTGATGCAATGA 780
DB 826 GAAACATCTCTGCTCTCATACGAAAGCCGTGAAATATCTGACTGATGCAATGA 885
QY 781 TGTGTTTATTTGGAACACATGGAAGAAATTTTACGCACTGCAAAACCAATTTCCAG 840
DB 886 TGTGTTTATTTGGAACACATGGAAGAAATTTTACGCACTGCAAAACCAATTTCCAG 945
QY 841 TGCAGAGAGACACTGTGTTTGTGATGATGTAATCAAAAAGTTATCTGCTAGAGGC 900
DB 946 TGCAGAGAGACACTGTGTTTGTGATGATGTAATCAAAAAGTTATCTGCTAGAGGC 1005
QY 901 GCATTTTATGACCGGTTGAGCAATGCACTTATTTGCAATTAAGAGGATTAATCT 960
DB 1006 TCAATTTATGATCTGTTGATTAAGATGCACTTATTTGCAATTAAGAGGATTAATCT 1065
QY 961 TAATTTTAAACAAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
DB 1066 TAATTTTAAACAAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1124
QY 1021 AAAGCAAGCTCAAAATTAAGAAATTAAGAAATTAAGAAATTAAGAAATTAAGAA 1048

```

DB 1125 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1152

RESULT 6  
AY566646 948 bp mRNA linear INV 22-MAR-2004  
LOCUS Polistes dominulus venom phospholipase A1 2 precursor mRNA, partial  
DEFINITION  
ACCESSION  
AY566646  
VERSION  
AY566646.1 GI:45510888  
KEYWORDS  
SOURCE  
ORGANISM  
Polistes dominulus (European paper wasp)  
Polistes dominulus  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;  
Vespididae; Vespidae; Polistinae; Polistes.  
REFERENCE  
Moawad T.I.S. and Hoffman, D.R.  
1 (bases 1 to 948)  
AUTHORS  
Direct Submission  
TITLE  
Submitted (05-MAR-2004) Pathology and Laboratory Medicine  
Department, Brody School of Medicine, East Carolina University, 600  
Moye Blvd., Greenville, NC 27858, USA  
JOURNAL  
Location/Qualifiers

## FEATURES

source

1..948  
/organism="Polistes dominulus"  
/mol\_type="mRNA"  
/db\_xref="taxon:34728"  
<1..>948  
/note="allergen Pol d 1.02"  
/codon\_start=1  
/product="venom phospholipase A1 2 precursor"  
/protein\_id="A567042.1"  
/db\_xref="GI:45510889"  
/translation="ADLLTLLRNGTLDRCITPDCTFNEKDIELHIVYSRDKRNGIILKK  
ELIKNYDLFOKSOISHQIALIHGFLSTGNNENPDMAALIEIDNPLVSYDMKSGA  
CNAPASTNVILVGSQAVGNTBRHGVKVAFTKLIVQVPSNIRLIGHISGATNSG  
PAGKEQRLKIKYKEIISLDPAKGSPLRNKPCPNRCETDAEYVQALHRSALIGVYN  
VGSVDYVYVNGSOPGCSFSCSHTAIVYLTCEIKRECCLLGTGPKMSYFTPKPLSQ  
CKRDTCVGVLANQSVPAKSPFVPEKDAFYCHNMGIDL"  
1..948  
/note="encodes venom phospholipase A1 2 proenzyme"  
40..948  
mat\_peptide  
/product="venom phospholipase A1 2"

## CDS

misc\_feature  
mat\_peptide  
/product="venom phospholipase A1 2"

## ORIGIN

Query Match 74.7%; Score 782.4; DB 3; Length 948;  
Best Local Similarity 89.3%; Pred. No. 7.2e-143;  
Matches 843; Conservative 0; Mismatches 101; Indels 0; Gaps 0;

```

QY 16 GATGATTCGACGACATTTGAAGAAATGATACCTTGAATGAGGCACTGCTCCGATTTGACT 75
DB 4 GATGATTTGACCACTCGTGAAGAAATGATACCTTGAAGAGGCACTCGGATTTGACT 63
QY 76 TTTAATGAGAAAGATATGATGATTTCTATGTTTCTCAAGGATATGAGGATGATGATTT 135
DB 64 TTTAATGAGAAAGATATGATGATTTCTATGTTTCTCAAGGATATGAGGATGATGATTT 123
QY 136 CTTAAGAAAGAACTTTAAGAAATGATGATGATTTCTCAAGGATATGAGGATATGAGGAT 195
DB 124 CTTAAGAAAGAACTTTAAGAAATGATGATGATTTCTCAAGGATATGAGGATATGAGGAT 183
QY 196 GTTGTATTTCTTATACAGGTTTCTTCACTGCGAATATGAGAAACTTCTGTTGCTATG 255
DB 184 ATTGCAATTTCTTATACAGGTTTCTTCACTGCGAATATGAGAAACTTCTGTTGCTATG 243
QY 256 TCGAAAGCTTTATATGAGAAAGATGATTTCTTGTATTTCCGTGACATGGAAGAGGT 315
DB 244 GCGAAAGCTTTATATGAGAAAGATGATTTCTTGTATTTCCGTGACATGGAAGAGGT 303
QY 316 GCTTGTATGCTTTTGTCTTCAAGAAAGATGCTTTGGTTATTTCCAAAGCCGTTGGAAC 375
DB 304 GCTTGTATGCTTTTGTCTTCAAGAAAGATGATTTGGTTATTTCCAAAGCCGTTGGAAC 363

```

OY		376	ACAGCTCAGCTTGGAAAAATTTTGTCAGTCAATTTTACAAGAACTGCTGTGAAGAAAATATAAA	433
Db		364	ACAGCTCACGTTGGAAAAATATGACTGATTTTTACAAAATTATTAAGAACAAATATAAA	423
OY		436	GTCGTGATATCAAAATATACGATTGATCCGGGCATAGTTTGCGCGCATATCTTCAGTTT	495
Db		424	GTGCCGATGCTGGAATATACGATTGATCGGCCATATGTTGGTGGCGCATATCTTCAGTTT	483
OY		496	CGCGGAAAAAGAACTTCAAAGTTAAATTTAGAAAAATACAGAAGAAATTAATCGGCTTGAT	555
Db		484	GCAGGAAAAAGAACTTCAAAGTTAAATTTAGAAAAATTAAGAAATTAATCGGCTTGAT	543
OY		556	CCTGTGACCGGATTTTTCATCGGAGTACGTCCGGACAGACTTTGGGTAAACAGACGCA	615
Db		544	CTGTGTGACCGGCTTTTCTTCAACGATTAAGTCCAACAGACTTTGGGAAACAGACGCA	603
OY		616	GAATATGTTCAAGTTATACATACATCAATCATATTAGAGATATATTATATGTTGTAGC	675
Db		604	GAATATGTTCAAGCTATACATACATCAACCATTATTAGAGATATATTATTAAGCTTGTAGC	663
OY		676	GTTGATTTCTACGTGAATTAATGAAAAAATCAACTGTGTCGAATGAACATCCTGCTCT	735
Db		664	GTTGATTTTTCAGTGAATTAATGAAAAAAGTCAACTGTGTCAGAGAACATCCTGTTCT	723
OY		736	CATCGAAGCGCTGAANAATATCTGACGTAGGACATAAACAATGAATGTTGTTTAATGGA	795
Db		724	CATCGAAGCGCTGAANAATATCTGACGTAGTATAAACAATGAATGTTGTTTAATGGA	783
OY		796	ACACCATGGAAGAAATATTTCAGCACTCCAAAACCAATTTCCCAGTCAGAGAGACACCC	855
Db		784	ACACCATGGAAGAGTTATTATTAGCAGCGCAAAACCAATTTCTCACTGAAAAAGACACCC	843
OY		856	TGTGTTTTCGTTGATGAATGCAAAAAAGTTATCCTGCTAGAGGCGCATTTTAATGACCG	915
Db		844	TGTGTTTTCGTTGACATGACGCTCAAGTTATCCTGCTAAAGGCTCATTTTAATGACT	903
OY		916	GTTGAAGCAATGACCTTATTGTCATACAGAGGAGATTAACT	959
Db		904	GTTGAANAAGTAGCCTTATTGGCATTAACAGAGCATTTAACT	947
<hr/>				
RESULT_7				
AY566647				
LOCUS		948 bp	mRNA	linear INV 22-MAR-2004
DEFINITION			Polistes dominulus venom phospholipase A1 3 precursor mRNA, partial cds.	
ACCESSION		AY566647		
VERSION		AY566647.1	GI:45510890	
KEYWORDS				
SOURCE				
ORGANISM			Polistes dominulus (European paper wasp)	
			Polistes dominulus	
			Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidae; Vespidae; Polistinae; Polistes.	
REFERENCE			1 (bases 1 to 948)	
AUTHORS			Moawad,T.I.S. and Hoffman,D.R.	
JOURNAL			Direct Submission	
			Submitted (05-MAR-2004) Pathology and Laboratory Medicine Department, Brody School of Medicine, East Carolina University, 600 Moye Blvd., Greenville, NC 27858, USA	
FEATURES			Location/Qualifiers	
source			1..948	
			/organism="Polistes dominulus"	
			/mol_type="mRNA"	
			/db_xref="taxon:34728"	
			<1..>948	
			/note="allergen Pol d 1.03"	
			/codon_start=1	
			/product="venom phospholipase A1 3 precursor"	
			/protein_id="AA567043.1"	
			/db_xref="GI:45510891"	
			/translation="ADULTIRUNGTLDRGTTTPDCTPNEKQIEHVSRDKRNGITLKK EILNKYLPRQSISHQIALIHGFISGTNNENPDAAKLIEIDNPLVTSVMKCA	

Query Match	74.4%	Score 779.2	DB 3	Length 948
Best Local Similarity	89.1%	Pred. No. 3,1e-142		
Matches	841	Conservative	0	Mismatches 103; Indels 0; Gaps 0;
misc_feature	1. .948 /note="encodes venom phospholipase A1 3 proenzyme"			
misc_deptide	40. .948 /product="venom phospholipase A1 3"			
ORIGIN				
Qy	16	GATGATTTCGACGACATTTAGAAATGTGACCTTGAAATAGAGCATGTCCTCGGATTGTACT	75	
Db	4	GATGATTTCGACGACCTTGAAATGTGACCTTGGAAGAGGATCACTCCGAGATTGTACT	63	
Qy	76	TTTAAATGAAAGATATAGTATTCTATGTTTACTCAAGGATTAAGGAGATGGTATTATT	135	
Db	64	TTTATATAGAAAGATATTGAGCTACACGTTTACTCAAGGATTAAGGATTAAGTATTATT	123	
Qy	136	CTTAAGAAAGAAATTTTAAGAAATTTAGACTCTGTTTAAAGTCTCAATATCAAAACAA	195	
Db	124	CTTAAGAAAGAAATTTTAAGAAATTTAGACTCTGTTTCAAAATCTCAATATCAATCA	183	
Qy	196	GTTGTATTCTTATACATGGTTTCCTTCACTGGGAAATATGAAAACTTCGTGTATG	255	
Db	184	ATTGCATATTCTTATACATGGTTTCCTTCACTGGGAAATATGAAAAATTTGCATGCA	243	
Qy	256	TCGAAACCTTAAATAGAAAAAGATGATTTCTTGTAATTTCCGTTCGACTGGAAGAGGT	315	
Db	244	GCGAAACCTTGAATAGAAATAGATAATTTCTTGTAATTTCCGTTCGACTGGAAGAGGT	303	
Qy	316	GCTTGATATGCTTTGCTTCAACAAAGGATGCTTTGGGTATTTCCAAAGCCGTTGGAAAC	375	
Db	304	GCTTGCAATGCTTTGCTTCAACAAATGATGTTTGGGTATTTCCAAAGCCGTTGGAAAC	363	
Qy	376	ACAAGTCAGCTGGAAAAATTTGTAGCTGATTTTACAAACTCACTGTAGAAAAATATAA	435	
Db	364	ACAAGTCAGCTGGAAAAATTTGTAGCTGATTTTACAAATTTATAGTAGAACAAATATAA	423	
Qy	436	GTGCTGATTCAAATATATGATGATGCGGCAATGTTGGGCGCGCATCTTCAAGTTTT	495	
Db	424	GTGCGGATGTCGAATATATGATGATGCGGCAATGTTGGGCGCGCATCTTCAAGTTTT	483	
Qy	496	GCGGGAAGAAAGTCCAAAGTTAAAAATTAGAAAAATPACAGGAATTTATCCGGCTTGAT	555	
Db	484	GCAAGAAAGAAAGTCCAAAGTTAAAAATTAGAAAAATPACAGGAATTTATCCGGCTTGAT	543	
Qy	556	CTGCTGGAACCGTATTTTCACTCGGAGTACTGTCCGGAACAGACTTTCGTAACAGACGA	615	
Db	544	CTGCTGGAACCGTCTTTTCTAACGAGTAATGTCCAGATATGATTTGTCCAAACAGACGA	603	
Qy	616	GAATATGTTCAAGTTATATACATCAATCAATATTAGAGTATATTATAATGTTGTAGC	675	
Db	604	GAATATGTTCAAGTTATATACATCAATCAATATTAGAGTATATTATAATGTTGTAGC	663	
Qy	676	GTTGATTTCTACGTGAATTTAGAAAAATCAACCTGTGTTGCAATGAACATCTCTGCTCT	735	
Db	664	GTTGATTTCTACGTGAATTTAGAAAAATCAACCTGTGTTGCAACCAATCTCTGCTCTCT	723	
Qy	736	CATACGAAGCCGTAAGAAATATCTGACTGAGTGCATTAACATGAATGTTGTTAAATTGA	795	
Db	724	CATACGAAGCCGTAAGAAATATCTGACTGAGTGCATTAACATGAATGTTGTTAAATTGA	783	
Qy	796	ACAACATGAAGAAATATTTCAGACTCCAAAACCAATTTCCAGTGCAGAGAGAGACACC	855	
Db	784	ACAACATGAAGAAATATTATTACAGCGCAAAACCAATTTCTCAGTGCAGAAAGAGACACC	843	
Qy	856	TGTGTTTGGCTGGATTGAATGCAAAAGTATCTGCTAGAGGCGCATTTTATGCACCG	915	
Db	844	TGTGTTTGGCTGGACTGCAACGCTCAAAAGTATCTGCTTAAGGCTCATTTTATGTACCT	903	



Db	304	GCTTGCAATGCTTTTGGCTTCAACTAATGATGTTTGGGTTACTCCCAAGCCGTTGGAAC	363
Qy	376	ACACGTCACGTTGGAAAAATTTGAGCTGATTTTACAAAACACTACTTTAGAAAAATATPAA	435
Db	364	ACAGCTCACGTTGGAAAAATATGATGCTGATTTTCAAAAATTAATAGTAGAAACAATATPAA	423
Qy	436	GTGCTGATATTAATATATACATATGATGCGGCAATGTTGGGCGGGCATTACTTCAGTTTT	495
Db	424	GTGCCGATGTCGAAATATACGATATATGCGCATATGTTGGGTGGCAATCTTCAGGTTTT	483
Qy	496	GCGGGAAAAAGAGTTCAAAAGTTTAAATTTAGGAAATATACAAAGAAATTAATCGGCTTGAT	555
Db	484	GCAGAAAAAGAGTTCCAAAGTTTAAATTTAGGAAATATATAGGAAATATATGCGGCTTGAT	543
Qy	556	CCTGCTGGAACCGTATTTTTCATCGGAGTGACTGTCCGACAGACTTTGCGTAAACAGCGCA	615
Db	544	CCTGCTGGAACCGTCTTTTCTTCTTAACGAGTAAATATGTCAGATGATTGTGGGAAACAGACGA	603
Qy	616	GAATATGTTCAAGTTATATACATCACTCAATCATATTAGAGATATTTATATGTTGTGATGC	675
Db	604	GAATATGTTCAAGCTATATACATCACTCAAGCCATATTTAGAGATATTTATACGTTGTGATGC	663
Qy	676	GTGATATTTCTACGGAATTTATGSAAAAAATCAACTGSGTTCATGTAACCATCCTGCTCT	735
Db	664	GTGATATTTTTCAGGAATTTATGSAAAAAATCAACTGSGTTCGACGGAACCATCTGTTCT	723
Qy	736	CATACGAAGCCGTGAATAATCTGACTGAGTGACATATAAACAATGAATGTTTAAATTTGA	795
Db	724	CATACGAAGCCGTGAATAATCTGACTGAGTGATATAAAGTGAATGTTTAAATTTGGA	783
Qy	796	ACACCATGAAAGAAATATTTTCAGCATCTCCAAACCAATTTCCAGTCCAGAGAGACACC	855
Db	784	ACACCATGAAAGAAATTTTATTTTATGAGCACCCCAAAATCAATTTCTCAGTCCAAAGAGACACC	843
Qy	856	TGTCGTTTGCGCTGGATTTGAATGCAAAAAGTATCCCTCTAGAGCGCATTTTATGACCG	915
Db	844	TGTCGTTTGCGCTGGACTGGAACGTCGCAAGTATCTCTGTAAGGCTCAATTTATGTAAGCT	903
Qy	916	GTTGAGCAAAATGACACCTTATTTGCCATATACGAGGGGATTTAAACT	959
Db	904	GTTGAAAAAGATGACCTTATTTGTCATATACGAAAGCATTTAAACT	947
RESULT 9			
ARI62936			
LOCUS	ARI62936	1050 bp	DNA
DEFINITION	Sequence 16 from patent US 6270763.	linear	PAT 17-OCT-2001
ACCESSION	ARI62936		
VERSION	ARI62936.1	GI:16233392	
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 1050)		
TITLE	King, T. Piao.		
FEATURES	Cloning and recombinant production of vespid venom phospholipases, and immunological therapies based thereon		
FEATURES	Patent: US 6270763-A 16 07-AUG-2001;		
SOURCE	Location/Qualifiers		
	1..1050		
ORIGIN	/organism="unknown"		
	/mol_type="unassigned DNA"		
Query Match	42.1%;	Score 441;	DB 6; Length 1050;
Best Local Similarity	67.0%;	Pred. No. 3.6e-76;	
Matches 665;	Conservative 0;	Mismatches 310;	Indels 18; Gaps 2;
Qy	65	CGGATTTGACTTTTAAATGAGAAAGATATATAGATTCATGTTTAACTCAAGGAGATTAAGGAG	124
Db	56	CGGATGTCCTTTATGATATGATACAGTTAAGATGATTTTATTTTAAACAGGGAACCCGAA	115





Db 236 TCGTTCCTAATGTCAGAGGCTCTTATGCAATACAGGTATTTCTTAAATATATGTCGATT 295  
 QY 305 GGAAGAAGGGTGGCTTAAATGCTTTTGTCTTCAACAAAGATGTTGGGTATTCCTCAAG 364  
 Db 296 GGGGATGGCTGCTTACTGATGAATACCCAGGCTGGAATATATGTTTATATAGGCTG 355  
 QY 365 CCGTTGAAAACACACGCTCAAGTTGAAAATTTGACCTGATTTTACAAAATCTATGTA 424  
 Db 356 CCGTGTATATACAGCTTATGGAATTTTATGCTATGATCGAAGAAACTTGAG 415  
 QY 425 AAAAATATTAAGCTGATATCAATATACGATTATCGGGCATGTTGGCGCCAT 484  
 Db 416 AACAAATATTAAGCCGATGACAAATATACACTGGTGGGACACATTTGGCGCACACA 475  
 QY 485 CTTCAGATTTTGGGAAAAAGAGTCAAAAGTTAAATTAAGAAATACAGAAATTA 544  
 Db 476 TTTCAGATTTTCAGAGCAAAAGATTCAGAGTTAAATTAAGAAATTTTCTGAATTA 535  
 QY 545 TCGGGCTTATCCGTGTCAGCCGATTTTTCATCGAGTCACTGCCGACAGACTTTGG 604  
 Db 536 TTGGGCTTATCCTGCTGGGCTAGTTTCAAGAAATATGTTCTCGAAGAAATCTGG 595  
 QY 605 TAAACAGCAGCAATATGTTCAAGTTATACATCATCAATCATATTAGAGATATTATA 664  
 Db 596 AGACAGACGCACTATATGTAACAATTTTACATCATCGACATTTAGGAACAGAGAA 655  
 QY 665 ATGTTGGTGGCTGATTTCTACGTAATTAATGAAAAAATCAAGCTGGTGC----- 717  
 Db 656 CTCTTGGACCGTGCATTTCTACATATTAACGAAATATCAACCGGTTGAGATATA 715  
 QY 718 --AATGAACATCTCTCTCATACGAAACCGTGAATATCTGACTGATGATTAAC 775  
 Db 716 TTATGAGAAATCTGCTCTCATACGAGCGGTGAATATCTTACGAGTGCATAGAC 775  
 QY 776 ATGAATGTTGTTAATTTGGAACCACTGGAAGAAATTTTACGACTCCAAACCAATT 835  
 Db 776 GCGAAATGTTTAAATTTGGGTTCC-----GCAATCCAGAAATCCGACCTGTT 826  
 QY 836 CCAGTGCAGAGAGACACCTGTTGTTGGTTGGAATGAATGCAAAAGTTATCCGTA 895  
 Db 827 CGAATGTCACAGAAACGAGTGGTTGGTTGAATTAACGAAAGAAATATCTTA 886  
 QY 896 GAGGCGCATTTTATGACCGGTTGAAGCAATGCACTTATGCCATAACGAGGGATTA 955  
 Db 887 GGGGCTCATTTATGATACCGGTTGAAGCTGCAATGTCATATGCAATTAACAAGGAAA 946  
 QY 956 AACTTAAATTAATTAACAAAGTCAATGTAACAAATATGATCTATGTAATTTAA 1015  
 Db 947 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1006  
 QY 1016 TGAATTAACGAAACAGTCAATTAATTAATTAATTAATTAATTAATTAATTA 1048  
 Db 1007 TGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1039  
 RESULT 13  
 LOCUS AR206926 1050 bp DNA linear PART 20-JUN-2002  
 DEFINITION Sequence 16 from patent US 6372471.  
 ACCESSION AR206926  
 VERSION AR206926.1 GI:21505676  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE Unclassified.  
 AUTHORS 1 (bases 1 to 1050)  
 TITLE King, T. Piao.  
 Cloning and recombinant production of vespid venom enzymes, such as phospholipase and hyaluronidase, and immunological therapies based thereon  
 Patent: US 6372471-A 16 16-APR-2002;  
 FEATURES  
 location/Qualifiers  
 1..1050  
 source

ORIGIN  
 /organism="unknown"  
 /mol\_type="unassigned DNA"  
 Query Match 42.1%; Score 441; DB 6; Length 1050;  
 Best Local Similarity 67.0%; Pred. No. 3, 6e-76;  
 Matches 665; Conservative 0; Mismatches 310; Indels 18; Gaps 2;  
 QY 65 CGGATGTACTTTATGAGAAAGATATGATTTCTATGTTTACTCAAGGGGTAAGCGAG 124  
 Db 56 CGTATGTCCTTTATGATATGATATGATACGTTAAGATATTTTAAACAAGGAAACCGAA 115  
 QY 125 ATGATATTAATCTTAAGAAAGAACTTTAACAATTAACGATCTGTTTCAAGTCTACA 184  
 Db 116 AACATGATTTTATACGCTAGTATACATGAACAGGCAATTAATTAAGAGTCAATCA 175  
 QY 185 TATCAAAACAAATGATATTTCTTAATACATGTTTCTTTCAACCTGGGATTAATGA 244  
 Db 176 TAAACGTCCAGTTGATTCATTTACGATGTTTACTTCGCTCAACCGAAATAATTT 235  
 QY 245 TCGTGTATGTCGAAAGCTTTAATAGAAAAAGATTTTCTGTAATTTCCGTGACT 304  
 Db 236 TCGTGTCTATGTCAGAGGCTCTTATGCAATACAGTGAATTTCTTAATATATGTCGAT 295  
 QY 305 GGAAGAAGGGTCTGTATATGCTTTGCTTCAACAAAGATCTTGGGTTATTCCTCAAG 364  
 Db 296 GGGGATGGCTGCTTGTACTGATGAATCCAGCTGTAAGTATGTTTATAGGCTG 355  
 QY 365 CCGTTGAAAACACACGTCACGTTGAAAAATTTGACTGATTTTCAAAACTACTTTGAG 424  
 Db 356 CCGTTGATATACAGCTTATGTTGGAATTTTATGCTATGATCCGAAAGAACTTTGAG 415  
 QY 425 AAAAATTAATTAAGTCTGATATCAATATACATTAATGCGGATGTTGGCGGCGATA 484  
 Db 416 AACAAATTAATTAAGTCCGATGACAAATATACGCTGTGGGACAGTTTGGCGCACACA 475  
 QY 485 CTTCAGATTTTGGGAAAAAGAGTTCAAAGTTTAAATTAAGAAATATCAAGAAATTA 544  
 Db 476 TTTCAGATTTTCCAGAGCAAAAGATTCAGAGTTTAAATTAAGAAATTTTCTGAATTA 535  
 QY 545 TCGGCTTGTATCTCTGACCGGATTTTTCATCGAGTCACTGCCGACAGACTTTGG 604  
 Db 536 TTGGGCTTATCTCTGAGCGCTTATGTTTCAAGAAATTAATGATGTTCCAGAGAAATCTCG 595  
 QY 605 TAAACAGCAGCAATATGTTCAAGTTATACATCATCAATCATATTAGAGATATTATA 664  
 Db 596 AGACAGACGCACTATATGTAACAATTTTACATCATCGACATTTAGGAACAGAGAA 655  
 QY 665 ATGTTGGTGGCTGATTTCTACGTAATTAATGAAAAAATCAACCTGGTGC----- 717  
 Db 656 CTCTTGGACCGTGCATTTCTACATTAATTAACGAAAGTATCAACCGGTTGCAATATA 715  
 QY 718 --AATGAACATCTCTCTCATACGAAACCGTGAATATCTGACTGATGATTAAC 775  
 Db 716 TTATGAGAAAACTTCTCTCATACGAGCGGTGAATATCTTTACGAGTGCATTAAGAC 775  
 QY 776 ATGAATGTTGTTAATTTGGAACACCATGGAAGAAATTTTACGACTCCAAACCAATT 835  
 Db 776 GCGAAATGTTTAAATTTGGGTTCC-----GCAATCCAGAAATCCGACCTGTT 826  
 QY 836 CCAGTGCAGAGAGACACTGTGTTGGTTGATGATTAATGCAAAAGATATCCGTGTA 895  
 Db 827 CGAATGTCACAGAAACGAGTGGCTTGGCTTGAATTAACGCAAAAGAAATATCTTA 886  
 QY 896 GAGGCGCATTTTATGACCGGTTGAAGCAATGCACTTATTTGCAATACAGAGGGATTA 955  
 Db 887 GGGGCTCATTTTATATGACCGGTTGAAGCTGCAATTTGCAATTAACAACGAGGAAA 946  
 QY 956 AACTTAAATTAATTAACAAAGTCAATGTAACAAATATGATCTATGTAATTTAA 1015  
 Db 947 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1006  
 QY 1016 TGAATTAACGAAACAGTCAATTAATTAATTAATTAATTAATTAATTAATTA 1048



TITLE Cloning and recombinant production of vespid venom phospholipases,  
and immunological therapies based thereon  
JOURNAL Patent: US 6270763-A 26 07-AUG-2001;  
FEATURES Location/Qualifiers  
source 1. .1341  
/organism="unknown"  
/mol\_type="unassigned DNA"

## ORIGIN

Query Match 40 7%; Score 426.2; DB 6; Length 1341;  
Best Local Similarity 66.9%; Pred. No. 2.7e-73;  
Matches 660; Conservative 0; Mismatches 308; Indels 19; Gaps 3;

```

QY 64 CCGATTTGATCTTTTATGAGAAAGATATATGATTTCTATGTTTACTCAAGGATAAGCGA 123
DB 156 CCCAATGTCCTTTTATTCGTATACAGTTTCGATATATTGAAACAAAGGAAAAACGA 215
QY 124 GATGTTATTTCTTAAGAAAGAACTTTACGAATTACGATCTGTTTACAAAGCTTACA 183
DB 216 AATCGTATCTTTATACACTACAGACATTACAGAAATCATCTGAATTTAAGAAAAAACT 275
QY 184 ATATCAAAACAGTTGATTTCTTATACAGGTTTCTTCAACGGAATATGAAAC 243
DB 276 ATPACACGTCAGTTGATTCATTACACAGGTTTACTTCACTGCAAGTGAACAAAT 335
QY 244 TTGTTGCTATGTCGAAGCTTTAATAGAAAAAGATTTTCTGTAATTCGGTCAC 303
DB 336 TTCATTAATTTGCAAAAGCTTTGTCAGTAAAGATTAATATGTTATCTCAATCGAT 395
QY 304 TGGAGAGAGGTCCTTTGATATGCTTTGCTTCAACAAAGATGCTTGGGTTATTCGAA 363
DB 396 TGGCAGACCGCTGCTGTAATGAAGCTTGAAGCTTGAAGTATTATATATCTACT 455
QY 364 GCGTTGGAACACACGTCAGCTGGAATTTGATGCTGATTTTACAAACTACTGTA 423
DB 456 GCTGCTAGAAATACAGTTTATGTCACATATATCGTACATTAACCAAGAACTCGTA 515
QY 424 GAAAAATATAAGTCGTATATCAATATACATGATGATGCGGATGTTGGCGGCAT 483
DB 516 AAAACCTATAAATCTCGATGCAAAATATACGATTAATGACATAGCTTAGAGCACAT 575
QY 484 ACTTCAGGTTTGGGGAAGAAAGATTCAAAGTTAAATTAAGAAAAATACAGGAAT 543
DB 576 GCTTACAGTTTTCAGGCAAAAGGTTCAAGATTAAATTAAGAAAAATATTCGAAAT 635
QY 544 ATCGGCTGATCCGTCGTCGACGATTTTCATCGGAGTACGTCGCGACGACTTGC 603
DB 636 ATTGGCTTGATCTGCTAGGCTTCGTCGATTCAAATCATTTGTCGAAAGACTCTGC 695
QY 604 GTAACAGACGCAATATGTTCAAGTTATACATACATCAATCATATTAAGAGTATTTAT 663
DB 696 GAGACGATGCAAGATATGTTCAAAATTAATACATACATCAAACTATTTAGAACCGAAAA 755
QY 664 AATGTTGTCGCTGATTTCTACGTAATTAAGAAAAATCAACTGTTGCAATGAA 723
DB 756 ACCCTTGTACCGTCAATTTCTACATGAATTAACGAAAGAAATCAACTGTTGCGGTAGA 815
QY 724 CCATCC-----TGCTCTCATCGAAAGCGTGAATATCTGACGAGTCATPAAA 774
DB 816 TTTTCTCGAAGTTTGCTCTCATTCGAGAGCGTGATATACATGCGTAGTCATPAAA 875
QY 775 CATGATGTTGTTTATTTGAAACACCATGGAAGAAATATTTCAAGCATCCAAACCAAT 834
DB 876 CACGATGTTGTTTATTTGGAATCC-----GAAGTCAAGAGTTCCGACGCTATT 926
QY 835 TCCCAATGCAAGAGACACTGTTGTTGCTTGAATGATGCAAAAAAGTTATCTGCT 894
DB 927 TCGTGTGCAAAACAGAGTGCCTTTCGTTGATTAACGCAAGAGTATACTAGT 986
QY 895 AGAGCGCATTTTATGACACCGGTTGAAGCAATGCACTTATTTGCCATPACGAGGGAT 954
DB 987 AAGGCTCATTTTATGATCCGGTGAAGGATCTGTTCTTTTTCATTAACAAAGGGAAG 1046

```

```

QY 955 AACTTTAATTAACAAAGTCATGTACCAAAAAATGATCTATTGATGATATATTAA 1014
DB 1047 ATTAATTAATTAATTAATAAAAGT-AATTTCAATTCATGGAATGATTTGTTAATGTCG 1105
QY 1015 ATGAATTAACGAACGTCAAATPAAAA 1041
DB 1106 ATGAATTAATTAATTCATTTAACCAATTA 1132

```

Search completed: April 28, 2005, 21:42:45  
Job time : 4897 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 27, 2005, 12:34:46 ; Search time 168 Seconds

(without alignments)  
736.686 Million cell updates/sec

Title: US-10-688-011-2

Perfect score: 1721  
Sequence: 1 ICFLDDSTFRNGTLNRGM.....AFYAPVEANAPYCHNEGIRL 320

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq.16Dec04:\*

1: geneseqp1980s:\*  
2: geneseqp1980s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1721	100.0	320	3 AAY84613	AAY84613 Amino aci
2	873.5	50.8	336	2 AAY25646	AAY25646 Vesputa s
3	873.5	50.8	336	7 ADC34895	ADC34895 Waep alle
4	866	50.3	317	2 AAR60599	AAR60599 Horneet ph
5	864	50.2	300	2 AAY25645	AAY25645 Vesputa s
6	864	50.2	300	7 ADC34894	ADC34894 Waep alle
7	856	49.7	300	2 AAR60603	AAR60603 Yellowjac
8	354	20.6	407	7 ADI23670	ADI23670 Mouse LPD
9	354	20.6	423	7 ADI23668	ADI23668 Mouse LPD
10	342.5	19.9	676	4 ABB62247	ABB62247 Drosophi1
11	340.5	19.8	460	7 ADI23666	ADI23666 Human LPD
12	339	19.7	415	5 ABB78294	ABB78294 Amino aci
13	339	19.7	460	5 AAO14803	AAO14803 phospholi
14	339	19.7	460	7 ABM79013	ABM79013 Human lip
15	339	19.7	481	5 AAO14804	AAO14804 phospholi
16	339	19.7	489	5 AAU99734	AAU99734 Long form
17	339	19.5	489	7 ABM79014	ABM79014 Human lip
18	336	19.5	319	2 AAR30739	AAR30739 C-termina
19	336	19.5	452	2 AAR30737	AAR30737 Guinea pi
20	327	19.0	470	2 AAR30741	AAR30741 GPI(+ ) mu
21	326	18.9	319	2 AAR34292	AAR34292 C-termina
22	323.5	18.8	540	4 ABB61963	ABB61963 Drosophi1
23	322	18.7	451	4 AAB73560	AAB73560 Human lip
24	322	18.7	451	4 AAE10996	AAE10996 Human lip
25	322	18.7	451	5 ABB06316	ABB06316 Human pho

26	322	18.7	451	6 ABU08952	ABU08952 Human nov
27	322	18.7	451	6 ADA83794	ADA83794 Human pho
28	322	18.7	451	7 ADI23676	ADI23676 Human LPD
29	322	18.7	451	7 ADI23674	ADI23674 Human LPD
30	322	18.7	451	8 ADR90482	ADR90482 Human pho
31	322	18.7	452	5 AAE17316	AAE17316 Human lip
32	320.5	18.6	451	7 ADI23672	ADI23672 Mouse LPD
33	318	18.5	432	2 AAR34294	AAR34294 HPL(- ) mu
34	311.5	18.1	339	4 ABB62229	ABB62229 Drosophi1
35	311.5	18.1	353	2 AAW59790	AAW59790 Amino aci
36	311.5	18.1	353	3 AAB19176	AAB19176 A partial
37	311.5	18.1	354	2 AAW59791	AAW59791 Amino aci
38	311.5	18.1	354	2 AAY41711	AAY41711 Human PRO
39	311.5	18.1	354	3 AAB44267	AAB44267 Human PRO
40	311.5	18.1	354	3 AAB24413	AAB24413 Human PRO
41	311.5	18.1	354	3 AAB19177	AAB19177 Human lip
42	311.5	18.1	354	4 AAU12371	AAU12371 Human PRO
43	311.5	18.1	354	4 AAB49892	AAB49892 Human PRO
44	311.5	18.1	354	4 AAB50912	AAB50912 Human PRO
45	311.5	18.1	354	6 ABO17815	ABO17815 Novel hum

## ALIGNMENTS

RESULT 1	
AAY84613	AAY84613 standard; protein; 320 AA.
ID	
AC	AAY84613;
XX	
DT	25-JUL-2000 (first entry)
XX	
DE	Amino acid sequence of a Pol a venom phospholipase A1 polypeptide.
XX	
KM	Pol a venom; phospholipase A1; paper wasp; immune response; immunogen;
KW	vespid venom; allergen-specific allergy; hymenoptera venom;
KW	autoimmune condition; allergic condition; viral infection; HIV;
KW	human immunodeficiency virus; Herpes Simplex virus; papilloma virus.
XX	
OS	Polistes annularis.
XX	
FH	Key
FT	Peptide
XX	
XX	Location/Qualifiers
XX	1..18 /note= "signal peptide"
XX	
PN	WO200018896-A1.
XX	
PD	06-Apr-2000.
XX	
XX	01-OCT-1999; 99WO-US023211.
XX	
XX	01-OCT-1998; 98US-00166205.
XX	
PA	(UYRQ ) UNIV ROCKEFELLER.
XX	
PI	King TP;
XX	
XX	WPI; 2000-293139/25.
DR	N-PSDB; AAA12616.
XX	
PT	New nucleic acids encode enzymes of wasp venom, are useful to treat
PT	insect sting allergy or immune system-related disorders and differ from
XX	the genomic sequences in that introns have been removed.
XX	
PS	Claim 4; Fig 1; 72pp; English.
XX	
CC	The present sequence represents Pol a venom phospholipase A1 polypeptide,
CC	isolated from the paper wasp. The enzyme acts on phospholipid substrates,
CC	e.g. to hydrolyse fatty acids. The recombinant Polistinae venom is used
CC	to modulate an immune response to an immunogen in a mammal, particularly
CC	a vespid venom allergen-specific allergy, or allergy to other hymenoptera
CC	venom. Alternatively the venom enzyme is used to treat an immunologically





PA (CIRC-) CIRCASSIA LTD.  
 XX Larche M, Ledger PW;  
 XX WPI; 2003-523267/49.  
 XX  
 PT Desensitizing an individual to a selected polypeptide antigen comprises  
 PT administering a composition containing polypeptide antigens in an amount  
 PT that generates a state of hyporesponsiveness to the antigen to allow  
 PT desensitization.  
 XX  
 PS Disclosure; Page 37; 57pp; English.  
 XX  
 CC The invention relates to a novel method for desensitizing an individual  
 CC to a selected polypeptide antigen. The method comprises administering a  
 CC composition that contains polypeptide antigens in an amount that  
 CC generates in the individual a state of hyporesponsiveness to the antigen  
 CC to allow desensitization to one or more polypeptide antigens. The method  
 CC of the invention has immunomodulator activity, and may have a use in gene  
 CC therapy. The composition and method are useful in manufacturing a  
 CC medicament for desensitizing an individual to a selected polypeptide  
 CC antigen or for generating in the individual a state of hyporesponsiveness  
 CC to the antigen to allow desensitization to one or more polypeptide  
 CC antigens. The present sequence is used in the exemplification of the  
 CC invention.  
 XX  
 SQ Sequence 336 AA;  
 XX  
 Query Match 50.8%; Score 873.5; DB 7; Length 336;  
 Best Local Similarity 52.0%; Pred. No. 4.9e-79;  
 Matches 166; Conservative 55; Mismatches 87; Indels 11; Gaps 4;  
 QY 2 CFLIDSTTRNGTLNRMGSDPTFNEKDIVFYVYSKDKGDIILKKEITLTVNDLFTKST 61  
 DB 23 CYGHDPLSYE---LDRG--PKCPFNSDVTWSIIETRENNRDLTYLTQLONHPEFKKXT 77  
 QY 62 ISKQVNLINGFLSTGNENNPNVMSKALIEKDDPLVIVSVMKKACNAFASTDALGYSK 121  
 DB 78 ITRPVVITHTGFTSSASSETNFINAKALVDDKNVMTVISIDWQTACTNEAGLKYLYPT 137  
 QY 122 AVGTRVNGKRVADFTKLVEKYKVLISNIRLIGSHGAHTSGPAGKEVQKLKGYKEI 181  
 DB 138 AANTRVNGVYIAITTKLVKHYKISMANIRLIGSHGAHTSGPAGKEVQKLKGYKEI 197  
 QY 182 IGLDPAGPYFHRSDCPRLCVTDAAEYVQVITHTSIIIGVYVNGSVDEYVYVNGXQPCN- 240  
 DB 198 IGLDPAPSPFDSNHSERLCETDAEYVQIHTSNYLTGTEKTLGTVDFYVNNNGKQPCGR 257  
 QY 241 --EBSCHTKAVKYLTCICIHGECCLIGTPMKKYSTFKPISQCHGDTCCVGLNAKSYPA 298  
 DB 258 FFSBVCVSHSRAVYIMACIRHCCCLIGIPKSK--SSQPISSCTKQECVGLNAKPYPS 314  
 QY 299 RGAFAVAVVEANAPYCHNEG 317  
 DB 315 RGSFYVVESTAPFCNNKG 333

RESULT 4  
 AAR60599  
 ID AAR60599 standard; protein; 317 AA.  
 XX  
 AC AAR60599;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 26-APR-1995 (first entry)  
 XX  
 DE Hornet phospholipase Dol ml.  
 XX  
 KM Hornet phospholipase; vespid venom enzyme, VV;  
 KM allergen-specific allergic condition; Dol ml.  
 XX  
 OS Dolichovespula maculata.  
 XX

PN W09420623-A1.  
 XX  
 XX PD 15-SEP-1994.  
 XX  
 XX PF 10-MAR-1994; 94WO-US002629.  
 XX  
 PR 11-MAR-1993; 93US-00031400.  
 PR 11-JAN-1994; 94US-00180209.  
 XX  
 PA (VVRQ ) UNIV ROCKEFELLER.  
 XX  
 PI King TP;  
 XX  
 DR WPI; 1994-303030/37.  
 DR N-PSDB; AAQ71520.  
 XX  
 PT Nucleic acid encoding vespid venom enzymes - used to produce polypeptides  
 PT for diagnosis and treatment of vespid venom allergen-specific allergic  
 PT conditions.  
 XX  
 PS Disclosure; Fig 1; 93pp; English.  
 XX  
 CC AAQ71520 is the cDNA sequence that codes for hornet phospholipase  
 CC (AAR60599), a vespid venom (VV) enzyme. These enzymes were used to  
 CC produce highly specific and individualised polypeptides for the diagnosis  
 CC and the treatment of VV-specific allergen specific conditions. For  
 CC CC therapy, the polypeptides or fragments can be administered by oral, nasal  
 CC or parenteral routes. (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 317 AA;  
 XX  
 Query Match 50.3%; Score 866; DB 2; Length 317;  
 Best Local Similarity 54.5%; Pred. No. 2.6e-78;  
 Matches 162; Conservative 42; Mismatches 87; Indels 6; Gaps 2;  
 QY 24 CTFNEKDIVFYVYSPDRDGIILKKEITLTVNDLFTKSTISKQVFLIHGFLSTGNNEFV 83  
 DB 21 CFPNSDVTVMKIFITREKRKADFTYLDIMARHNEFKSIIKRPVFTHTGFTSSATENFV 80  
 QY 84 AMSKALIEKDDPLVIVSVMKKACNAFASTDALGYSKAVGNTRHVGKRVADFTKLVEK 143  
 DB 81 AMSEALMHNTDFLIINWDMMACTDEYPELKMFPKAAAGNTRLVGNFIMLAKLVEQ 140  
 QY 144 KYVLISNIRLIGSHGAHTSGPAGKEVQKLKGYKEIIGLDPAGPYFHRSDCPRLCVT 203  
 DB 141 KYVPMNIRLIVGSHGSHGHTSGPAGKEVQKLKGYKEIIGLDPAGPSFKNDSEKICET 200  
 QY 204 DAEYVQVITHTSIIIGVYVNGSVDFYVYVNGXQPCN---EBSCHTKAVKYLTECIKHE 260  
 DB 201 DAHYVQILHTSSNLTGERTGTGVDFTYNNSSNPGCKYIIGTCSHRAVKYFTBCIRRE 260  
 QY 261 CCLIGTPWKYFSTPKPISQCHGDTCCVGLNAKSYPARGAFAPYVEANAPYCHNEG 317  
 DB 261 CCLIGVPOSK---NPQPVSKCTRNCECVGLNAKPKPKGSPFVPEAEAPYCNNG 314

RESULT 5  
 AAY25645  
 ID AAY25645 standard; protein; 300 AA.  
 XX  
 AC AAY25645;  
 XX  
 DT 30-SEP-1999 (first entry)  
 DT  
 XX  
 DE Vespula sp. allergen 1709545 Ves M 1 protein fragment.  
 XX  
 KM Major histocompatibility complex; class II; desensitizing; human;  
 KM allergen; grass; tree; weed; pollen; fungi; mould; food; insect; sting;  
 KM chironomidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee;  
 KM screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat;  
 KM cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;  
 KM mice; gerbil; vaccine; treatment; prevention; hypersensitivity; wasp.  
 XX



```

XX 25-MAR-2003 (revised)
DT 26-APR-1995 (first entry)
XX
XX Yellowjacket phospholipase.
DE
XX Yellowjacket phospholipase; vespid venom enzyme; VV;
KM allergen-specific allergic condition.
XX
XX Vesipula maculifrons.
OS
XX WO9420623-A1.
PN
XX 15-SEP-1994.
PD
XX 10-MAR-1994; 94WO-US002629.
PF
XX 11-MAR-1993; 93US-00031400.
PR 11-JAN-1994; 94US-00180209.
PR
XX (UYRQ ) UNIV ROCKEFELLER.
PA
XX King TP;
PI
XX WPI; 1994-303030/37.
DR N-PSDB; AAQ71523.
DR
XX Nucleic acid encoding vespid venom enzymes - used to produce polypeptides
PT for diagnosis and treatment of vespid venom allergen-specific allergic
XX conditions.
XX
XX Disclosure; Fig 5; 93pp; English.
PS
XX AAQ71523 is the cDNA sequence that codes for yellowjacket phospholipase
CC (AAR60603), a vespid venom (VV) enzyme. These enzymes were used to
CC produce highly specific and individualised polypeptides for the diagnosis
CC and the treatment of VV-specific allergen specific conditions. For
CC therapy, the polypeptides or fragments can be administered by oral, nasal
CC or parenteral routes. (Updated on 25-MAR-2003 to correct PN field.)
CC
XX
XX Sequence 300 AA;
SQ
Query Match 49.7%; Score 856; DB 2; Length 300;
Best Local Similarity 53.2%; Pred. No. 2.4e-77;
Matches 155; Conservative 51; Mismatches 83; Indels 6; Gaps 2;
QY 22 PDCTFNEKDVIVFYVSRDKDGIILKKEITLTYDLFTKSTISKOVFLHIGFLSTGNNEN 81
DB 2 PKCFPSNDTVSIIEETENNRDLYTQTLONHPEFKKITTREVVFIITGFTSSASETN 61
QY 82 FVAMSKALIEKDFLVISVDMKGCANAFSTKDALGYSKAVGNTRHVGFVADFTKLV 141
DB 62 FIMAKALVMDKDNMVISIDWQTAACITNEAAGLYLYVPTAARTRLVGYIATITQKLV 121
QY 142 EKKVVLISNIRLIGHSIGAHSTSGPAGKEVQKLGKXKEIIGLDPAPYFHRSCPRLC 201
DB 122 KHYKISPAIRLIGHSIGAHSGPAGKGVDELKLGKYSSEIIGLDPAPSPDSNHCSERLC 181
QY 202 VTDAEVYQVHTSIILGVYVNGSVDFYVYVGNQPCN--EPSCSHTRAVKYLTECIK 258
DB 182 ETDABEVQIILHTSNVLTGTEKTLGTVDFYMNNGKQPCGPFPSVCSHSAVYIMACIK 241
QY 259 HECCLLTTPWKKTFFSTKPIISQCRGDTCCVGLNAKYPARGAFYADVEANAPYCHNEG 317
DB 242 HECCLLTIGIPSK--SSQPISSCTKQECVCGLNAAKYTSRGSFYVVESTVPCKNKG 297

```

```

DT 06-MAY-2004 (first entry)
XX
XX Mouse LPDL #2.
DE
XX Lipase; LPDL; lipase deficiency; atherosclerosis;
KM fatty liver disease; dyslipidaemia; hypercholesterolaemia;
KM hypertriglyceridaemia; mixed dyslipidaemia; lipid deficient state;
KM lipoprotein deficient state; mouse; enzyme.
XX
XX Mus sp.
OS
XX WO2003055995-A2.
PN
XX 10-JUL-2003.
PD
XX 23-DEC-2002; 2002WO-CA001998.
PF
XX 21-DEC-2001; 2001US-0341786P.
PR 10-JAN-2002; 2002US-0346603P.
PR
XX (WENX/) WEN X.
PA (STEW/) STEWART A. K.
PA (TSUI/) TSUI L.
PA (HEGE/) HEGELE R. A.
XX
XX Men X, Stewart AK, Tsui L, Hegeler RA;
PI
XX WPI; 2003-569444/53.
DR N-PSDB; ADI23669.
DR
XX Novel isolated LPDL or LPDLR lipase polypeptides, useful for identifying
PT substances that bind to the protein and which are useful for treating
PT diseases associated with lipase function e.g. atherosclerosis and
XX hypercholesterolemia.
XX
XX Claim 2; SEQ ID NO 6; 172pp; English.
PS
XX The invention relates to an isolated mammalian (e.g., human or mouse)
CC lipase polypeptide (polyp), e.g., LPDL (I) or LPDLR polyp (II). (I) or
CC (II) is useful for identifying substances which can bind with LPDL or
CC LPDLR polyp, and for identifying a compound that affects the binding of
CC LPDL or LPDLR polyp and an LPDL or LPDLR binding polyp. (I) or (II) or
CC their nucleic acid is useful for identifying a compound that affects LPDL
CC or LPDLR polyp activity or expression. (I) or (II) or their nucleic acid
CC is useful for detecting or monitoring a condition associated with
CC increased or decreased LPDL or LPDLR expression or activity in an animal,
CC where the condition is lipase deficiency, atherosclerosis, fatty liver
CC disease and dyslipidaemia, such as hypercholesterolemia.
CC hypertriglyceridaemia, mixed (combined) dyslipidaemia, lipid or lipoprotein
CC deficient states, and/or any other tissue or plasma disorders of lipid or
CC lipoprotein metabolism. The nucleic acid is useful for diagnosing the
CC presence of or a predisposition for a disorder in a subject which
CC involves detecting a germline alteration in the nucleic acid in the
CC subject. An inhibitor is useful for modulating triglyceride activity by
CC inhibiting expression or activity of (I) or (II). The nucleic acid is
CC useful as a probe or primer. The present sequence is used in the
CC exemplification of the invention.
CC
XX
XX Sequence 407 AA;
SQ
Query Match 20.6%; Score 354; DB 7; Length 407;
Best Local Similarity 32.1%; Pred. No. 1.7e-26;
Matches 93; Conservative 44; Mismatches 109; Indels 44; Gaps 9;
QY 52 TNYDLFTKSTISKOVFLHIGFLSTGNNENFVA--MSKALIEKDFLVISVDMKGCANAF 110
DB 33 SNNSLNTRFNPACKTWTIIGHYRPGSTPWLRSFTKALPKQDVLIVDMQSGATTFM 92
QY 111 ASTKDALGYSKAVGNTRHVGFVADFTKLVK--YKVLISNIRLIGHSIGAHSGPAG 167
DB 93 -----YSRAVRNTRR-----VAEISRETIENLIGHSIGAHSGPAG 140
QY 168 KEVQKLGKXKEIIGLDPAPYFHRSDCEPRLCVDPAEVYQVYIHNSI-ILSVYVNGSV 226

```



CC sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-  
CC ABB72072). The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at [ftp.wipo.int/pub/published\\_pot\\_sequences](http://pub.int/pub/published_pot_sequences)  
XX  
SQ Sequence 676 AA;

**SQ** Sequence 676 AA;

Query Match	19.9%	Score 342.5	DB 4	Length 676
Best Local Similarity	30.1%	Pred. No. 5e-25		
Matches 93, Conservative	41	Mismatches 106	Indels 69	Gaps 10

[illegible]

## RESULT 11

ID ADI23666 standard; protein; 460 AA.

AC ADI23666 ;

DT 06-MAY-2004 (first entry)

## DE Human LPDL

KM lipase LPL; LPLR; lipase deficiency; atherosclerosis;  
KM fatty liver disease; dyslipidaemia; hypercholesterolaemia;  
KM hypertriglyceridaemia; mixed dyslipidaemia;  
KM lipoprotein deficient state; human; enzyme.

**Homo sapiens.**

PN WO2003055995-A2.

PD 10-JUL-2003.

PF 23-DEC-2002; 2002WO-CA001998.

PR 21-DEC-2001; 2001US-0341786P.  
PR 10-JAN-2002; 2002US-0346603P.

PA (WENX/) WEN X.  
PA (STEW/) STEWART A K  
PA (TSUI/) TSUI L.  
PA (HEGE/) HEGELE R A.

PI Wen X, Stewart AK, Tsui L, Hegele RA; ...

DR WPI; 2003-569444/53.  
DR N-PSDB; ADI23665.

PT Novel isolated LPDL or LPDLR lipase polypeptides, useful for identifying

PT substances that bind to the protein and which are useful for treating  
PT diseases associated with lipase function e.g. atherosclerosis and  
PT hypercholesterolemia.

PS Claim 2; SEQ ID NO 2; 172pp; English

The invention relates to an isolated mammalian e.g., human or mouse) lipase polypeptide (polyp), e.g., LPDL (I) or LPDL polyp (II), (I) or (II) is useful for identifying substances which can bind with LPDL or LPDL polyp, and for identifying a compound that affects the binding of LPDL or LPDL polyp and an LPDL or LPDL binding polyp. (I) or (II) or their nucleic acid is useful for identifying a compound that affects LPDL or LPDL polyp activity or expression. (I) or (II) or their nucleic acid is useful for detecting or monitoring a condition associated with increased or decreased LPDL or LPDL expression or activity in an animal, where the condition is lipase deficiency, atherosclerosis, fatty liver disease and dyslipidaemias, such as hypercholesterolemia, hypertriglyceridaemia, mixed (combined) dyslipidaemia, lipid or lipoprotein deficient states, and/or any other tissue or plasma disorders of lipid or lipoprotein metabolism. The nucleic acid is useful for diagnosing the presence of or a predisposition for a disorder in a subject which involves detecting a germline alteration in the nucleic acid in the subject. An inhibitor is useful for modulating triglyceride activity by inhibiting expression or activity of (I) or (II). The nucleic acid is useful as a probe or primer. The present sequence is used in the exemplification of the invention.

**SQ Sequence 460 AA;**

Query Match	19.8%	Score 340.5	DB 7	Length 460
Best Local Similarity	32.0%	Pred. No. 4.5e-25		
Matches 103; Conservative	43;	Mismatches 107;	Indels 69;	Gaps 14

Oy	4	RDGIIJKEKEL	----	TNYD	-----	LEFS	-----	-----	TISKOVLEFIHFLSTG	-----	N	79
			:	:	:	:	:	:		:	:	
Db	34	RDLFIIRIEIITLMYTRYNLCNAEPLFEQNNLSANNFNQKTIWLIHCRVYGSIPMLT										93
			:	:	:	:	:	:		:	:	
Oy	80	ENFVAMSKALIEKDEPLVITSVDWKGCACNAFASTDOLGYSKAVGNTRHVGFVADFTKL										13
			:	:	:	:	:	:		:	:	
Db	94	QNEV----	RIIMNEEDNNVIVIMWSRATPII						----	YNAVKNTRKVAVSLSHIKN		14
			:	:	:	:	:	:		:	:	
Oy	140	LVEKYKYLISNITLISHGIAHTSGAGKEVOKLKLKGYKEIIGDIPAGFYHRSDCPDR										19
			:	:	:	:	:	:		:	:	
Db	143	LT--KHGASLDNFHFIEVSLGSAHISGVG----	----	----	----	----	----	----	KIFHGQIGRTIGLDIPAGPRSRKPRPYR			19
			:	:	:	:	:	:		:	:	
Oy	200	LCVTDAYVOVIHT--SIIIGVYVNGSVDPFYVYNGNQPCCNEP-----	----	----	----	----	----	----	SCSHTKAV			25
			:	:	:	:	:	:		:	:	
Db	198	LDTYDAKFDVIVIHSDNSNGLIOEPLCHIDIPFYPRGKNQGGCKPSIFSGIOPIKCHORAV										25
			:	:	:	:	:	:		:	:	
Oy	251	KVLTCEKHECCJIGFPMKKY--FSTPKPDISOC-----	----	----	----	----	----	----	RQDTCVGNLAKASY			29
			:	:	:	:	:	:		:	:	
Db	258	HLTMASLEFNCAISIFPCRSYKDYKT-----	----	----	----	----	----	----	SICVDDCCFKKSKSRGLGQALFGCVLKE			31
			:	:	:	:	:	:		:	:	
Oy	297	-----	PARGAFYAVEANAPYC									313
			:	:	:	:	:	:		:	:	
Db	314	RMEGRPLRTTVPLDTSIGTYPC										335
			:	:	:	:	:	:		:	:	

## RESULT 12

ID ABB78294 standard; protein; 415 AA

AC ABB78294;

DT 05-DEC-2002 (first entry)

Amino acid sequence of lipid-associated molecule (LIPAM)-5.

KM Human; lipid-associated molecule; LIPM; cardiovascular disease;  
KM atherosclerosis; hypertension; aneurysm; congestive heart failure;  
KM angina pectoris; heart disease; lung disease; oedema; emphysema;  
KM bronchitis; gastrointestinal disease; nausea; peptic ulcer;  
KM Crohn's disease; lipid metabolism; Fabry's disease; diabetes mellitus

KM hyperlipidaemia; autoimmune disease; inflammatory disease;  
 KM acquired immunodeficiency syndrome; AIDS; anaemia; asthma; gout;  
 KM pancreatitis; neurological disease; stroke; Alzheimer's disease;  
 KM multiple sclerosis; Parkinson's disease; anxiety; schizophrenia; amnesia;  
 KM metabolic disease; Addison's disease; developmental disease;  
 KM Cushing's syndrome; endocrine disease; cell proliferative disorder;  
 KM cancer; leukemia; lymphoma; sarcoma.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 18 /note= "potential glycosylation site"  
 FT Modified-site 27 /note= "potential phosphorylation site"  
 FT Modified-site 84 /note= "potential phosphorylation site"  
 FT Modified-site 106.134 /note= "potential phosphorylation site"  
 FT Domain /note= "transmembrane domain"  
 FT Modified-site 135 /note= "potential phosphorylation site"  
 FT Modified-site 145 /note= "potential phosphorylation site"  
 FT Modified-site 151 /note= "potential phosphorylation site"  
 FT Modified-site 232 /note= "potential phosphorylation site"  
 FT Modified-site 278.306 /note= "potential phosphorylation site"  
 FT Domain /note= "transmembrane domain"  
 FT Modified-site 304 /note= "potential phosphorylation site"  
 FT Modified-site 311 /note= "potential phosphorylation site"  
 FT Modified-site 351 /note= "potential phosphorylation site"  
 FT Modified-site 371 /note= "potential glycosylation site"  
 FT Modified-site 411 /note= "potential phosphorylation site"  
 FT Modified-site /note= "potential phosphorylation site"  
 XX  
 PN MO200263005-A2.  
 XX  
 PD 15-AUG-2002.  
 XX  
 PF 06-FEB-2002; 2002MO-US003813.  
 XX  
 PR 06-FEB-2001; 2001US-0266910P.  
 PR 16-MAR-2001; 2001US-0276855P.  
 PR 16-MAR-2001; 2001US-0276891P.  
 PR 28-MAR-2001; 2001US-0279760P.  
 PR 13-APR-2001; 2001US-0283818P.  
 PR 20-APR-2001; 2001US-0285405P.  
 XX  
 PA (INCY-) INCYTE GENOMICS INC.  
 XX  
 PI Das D, Yao MG, Arvizu C, Baughn MR, Lu Y, Hafalia AJA, Walla NK,  
 PI Griffin JA, Lu DM, Yue H, Ding L, Townley DJ, Elliott VS;  
 PI Forsythe I, Ramkumar J, Gandhi AR, Ison CH, Warren BA, Tang YT,  
 PI Emerling BM, Honchell CD;  
 XX  
 DR MPI; 2002-627558/67.  
 DR N-PSDB; ABV72131.  
 XX  
 PT New human lipid-associated molecules, useful for diagnosing, treating or  
 PT preventing cardiovascular disorders (e.g. aneurysms), neurological  
 PT disorders (e.g. Parkinson's disease) or cancers (e.g. leukemia or  
 PT lymphoma).  
 XX  
 PS Claim 1; Page 134-135; 152pp; English.  
 CC The present sequence represents a lipid-associated molecule (LIPAM).  
 CC LIPAM polypeptides, polynucleotides and agonists are useful for treating  
 CC a condition associated with decreased expression of functional LIPAM. The

CC antagonist is useful for treating a disease associated with  
 CC overexpression of functional LIPAM. The anti-LIPAM antibody is useful for  
 CC diagnosing a condition or disease associated with the expression of  
 CC LIPAM. The polypeptides, polynucleotides, agonists and antagonists may  
 CC also be used for preventing these diseases. These polypeptides,  
 CC polynucleotides, agonists and antagonists are particularly useful for  
 CC diagnosing, treating or preventing cardiovascular (e.g. atherosclerosis,  
 CC hypertension, aneurysms, congestive heart failure, angina pectoris, or  
 CC ischemic or rheumatic heart disease), lung (e.g. edema, emphysema or  
 CC bronchitis) gastrointestinal (e.g. nausea, peptic ulcer or Crohn's  
 CC disease), lipid metabolism (e.g. fatty acids disease, diabetes mellitus or  
 CC hyperlipidaemia), autoimmune/inflammatory (e.g. acquired immunodeficiency  
 CC syndrome (AIDS), anaemia, asthma, gout, pancreatitis or Crohn's disease),  
 CC neurological (e.g. stroke, Alzheimer's disease, multiple sclerosis,  
 CC Parkinson's disease, anxiety, schizophrenia or amnesia), metabolic (e.g.  
 CC Addison's disease), developmental (e.g. Cushing's syndrome), endocrine or  
 CC cell proliferative disorders (e.g. cancers including leukemia, lymphoma  
 CC or sarcoma)  
 XX  
 SQ Sequence 415 AA;  
 Query Match 19.7%; Score 339; DB 5; Length 415;  
 Best Local Similarity 32.8%; Pred. No. 5, 6e-25;  
 Matches 96; Conservative 38; Mismatches 107; Indels 52; Gaps 11;  
 QY 53 NYDLFTKSTISKQVFLHGFISTGN---NENFVMSKALIEKDDPLVYSYDMKKGACN 108  
 DB 18 NNSLVNFTQKKTWLVHGYRVSIPMLQNFV---RLNBEEMVYIVDMSGATT 74  
 QY 109 AFASTKDALGYSKAVGNTBHVGFVADFTKLIVKXKVLISNRLIGSLGHTSGFAG 168  
 DB 75 FI-----YRAVAVNTRKVAVSLSHVHKILL-KHGASLDNHFVIGVSLGHSFVG- 124  
 QY 169 EYQKLTGKXKELIGDPAGPFRHSDCEDRLCTPDAEVVOYIHT-SILGTYVNGSVD 227  
 DB 125 ---KIFHGQLGRITGLDPAGPRPSRPPYSLDYTDKAVDYIHSDSNGLGIOEPGLGID 181  
 QY 228 FVYVNGKNPGGNEP-----SCSHTKAVKVLFEICIKHECCLITPMKKY--FSTPKP 277  
 DB 182 FYPNGSNKPGCPKRSFSGIOTPKCNHQAIVLPMASLETNCFISFPKRSYKDYCT--- 238  
 QY 278 ISQC-----RGDTVCVGLNASKY-----PARGAFYAPVEANAPYC 313  
 DB 239 -SLCVDCDFCEKSCPRLTGYQAKLFKGLKERWGRPLRTYVFLDTSGTYPC 290  
 RESULT 13  
 ID AA014803  
 XX AA014803 standard; protein; 460 AA.  
 XX  
 AC AA014803;  
 XX  
 DT 08-UTL-2002 (first entry)  
 XX  
 DE Phospholipase A1 protein.  
 XX  
 KM Phospholipase A1; phospholipase inhibitor; phospholipase antagonist;  
 KM phospholipase potentiators; hypertension; cancer; blood diseases; wound.  
 XX  
 OS Unidentified.  
 OS  
 PN MO200231131-A1.  
 XX  
 PD 18-APR-2002.  
 XX  
 PF 20-AUG-2001; 2001MO-JP007106.  
 XX  
 PR 11-OCT-2000; 2000JP-00311015.  
 XX  
 PA (MOCH ) MOCHIDA PHARM CO LTD.  
 XX  
 PI Arai H, Aoki J;  
 XX

DR WPI; 2002-362678/39.  
 DR N-PSDB; AAL42566.  
 PT New phospholipase A1 having substrate specificity for phosphatidic acid,  
 PT useful in diagnosis and screening inhibitors, antagonists and  
 PT potentiators for treating e.g. hypertension.  
 XX  
 PS Claim 1; Fig 1-Fig 2; 60pp; Japanese.  
 XX  
 CC The invention comprises the amino acid and coding sequence of the  
 CC phospholipase A1. The phospholipase A1 DNA and protein sequences of the  
 CC invention are useful in diagnosis and screening of phospholipase  
 CC inhibitors, antagonists and potentiators for drug compositions which can  
 CC be used in treating hypertension, cancer, blood diseases and wounds. The  
 CC present amino acid sequence represents the phospholipase A1 protein of  
 CC the invention  
 CC  
 XX  
 SQ Sequence 460 AA;  
 Query Match 19.7%; Score 339; DB 5; Length 460;  
 Best Local Similarity 32.8%; Pred. No. 6.4e-25;  
 Matches 96; Conservative 38; Mismatches 107; Indels 52; Gaps 11;  
 QY 53 NYDLFTKSTISKQVFLIHGFLSTGN---NENFVAMSKALIEKDPFLVISVDMKKGACN 108  
 DB 63 NNSLNNVFNQKTKVLIHGRPVGSIPLMLQNFV---RLINBEDMNVIVDMSRGATT 119  
 QY 109 AFASTKDALGSKAVGNTRHVGKFAVDFTKLVEKRVKVLISNIRLIGHSGAHTSGFAGK 168  
 DB 120 FI-----YNRAVKNTRKVAVSLSVHINKLL-KHGASLDNFHFGISLGAHISGFVG- 169  
 QY 169 EVQKLLKGGKKEIIGDPPAGPYFHRSDCPRLCTDAEYQVYHT-SIIIGVYNNVSVD 227  
 DB 170 ---KIFHGQLGRITGLDPAGRPFRKPPYSRLDYTDKAFVDVHSDNGSLGIDEPGLAHID 226  
 QY 228 FYVNYGKNQPGCNBP-----SCSHTKAVKYLTECIKHECCCLIGTPMKKY--FSTPKP 277  
 DB 227 FYRNGKNKQPGCKPSISGIFQIKCNHQRVHLEFMALELNCNFIISPCSYDYDKT--- 283  
 QY 278 ISQC-----RGDTCCVCGVGNASKY-----PARGAFYAPVEANAPYC 313  
 DB 284 -SLCVDCCDFKEKSCPLGYQAKLFKGVLEKRMGRPLRTTVLDTSGTYPFC 335  
 RESULT 14  
 ID AAM79013 standard; protein; 460 AA.  
 XX AAM79013;  
 AC AAM79013;  
 DT 15-JAN-2004 (first entry)  
 XX  
 DE Human lipase.  
 XX  
 KM Human; lipase; modulator; screening; cytostatic; antidiabetic;  
 KM neuroprotective; nootropic; anticonvulsant; antiparkinsonian;  
 KM antiasthmatic; anorectic; cardiac; vasodilator; antiarrhythmic;  
 KM hypotensive; uteropathic; gene therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003072767-A2.  
 PD 04-SEP-2003.  
 XX  
 PF 26-FEB-2003; 2003WO-EP001940.  
 XX  
 PR 27-FEB-2002; 2002US-0359634P.  
 PR 12-MAR-2002; 2002US-0363101P.  
 PR 30-JUL-2002; 2002US-0399133P.  
 PR 15-AUG-2002; 2002US-0403360P.  
 XX  
 PA (FARB ) BAYER AG.

XX  
 PI Liou J;  
 XX  
 DR WPI; 2003-712728/67.  
 DR N-PSDB; ACF80618.  
 PT Human lipase polynucleotide and its encoded protein, useful for  
 PT identifying modulators of lipase activity and in gene therapy for  
 PT preventing or treating e.g. cancer, diabetes, Alzheimer's disease,  
 PT ischemia, asthma or obesity.  
 XX  
 PS Claim 1; Fig 2; 114pp; English.  
 XX  
 CC The present sequence is the protein sequence of human lipase. The  
 CC invention provides isolated polynucleotides which encode human lipase,  
 CC including the present sequence, as well as expression vectors, host cells  
 CC and methods of detecting the lipase polynucleotide and producing the  
 CC lipase polypeptide. The lipase polynucleotides and polypeptides are used  
 CC in claimed methods of screening for agents that decrease or regulate the  
 CC activity of the lipase. Such agents, or an expression vector containing a  
 CC lipase polynucleotide, can be used to modulate the activity of a lipase  
 CC in a disease, e.g. cancer, diabetes, a central nervous system disorder,  
 CC asthma, obesity, a cardiovascular disorder or a urological disorder  
 CC (claimed). The CNS disorder may include Alzheimer's disease, Parkinson's  
 CC disease or Huntington's disease. The cardiovascular disorder may include  
 CC myocardial infarction, ischaemia, arrhythmias or hypertension. The  
 CC urological disorder may include benign prostatic hyperplasia  
 CC  
 XX  
 SQ Sequence 460 AA;  
 Query Match 19.7%; Score 339; DB 7; Length 460;  
 Best Local Similarity 32.8%; Pred. No. 6.4e-25;  
 Matches 96; Conservative 38; Mismatches 107; Indels 52; Gaps 11;  
 QY 53 NYDLFTKSTISKQVFLIHGFLSTGN---NENFVAMSKALIEKDPFLVISVDMKKGACN 108  
 DB 63 NNSLNNVFNQKTKVLIHGRPVGSIPLMLQNFV---RLINBEDMNVIVDMSRGATT 119  
 QY 109 AFASTKDALGSKAVGNTRHVGKFAVDFTKLVEKRVKVLISNIRLIGHSGAHTSGFAGK 168  
 DB 120 FI-----YNRAVKNTRKVAVSLSVHINKLL-KHGASLDNFHFGISLGAHISGFVG- 169  
 QY 169 EVQKLLKGGKKEIIGDPPAGPYFHRSDCPRLCTDAEYQVYHT-SIIIGVYNNVSVD 227  
 DB 170 ---KIFHGQLGRITGLDPAGRPFRKPPYSRLDYTDKAFVDVHSDNGSLGIDEPGLAHID 226  
 QY 228 FYVNYGKNQPGCNBP-----SCSHTKAVKYLTECIKHECCCLIGTPMKKY--FSTPKP 277  
 DB 227 FYRNGKNKQPGCKPSISGIFQIKCNHQRVHLEFMALELNCNFIISPCSYDYDKT--- 283  
 QY 278 ISQC-----RGDTCCVCGVGNASKY-----PARGAFYAPVEANAPYC 313  
 DB 284 -SLCVDCCDFKEKSCPLGYQAKLFKGVLEKRMGRPLRTTVLDTSGTYPFC 335  
 RESULT 15  
 ID AAO14804 standard; protein; 481 AA.  
 XX AAO14804  
 AC AAO14804;  
 DT 08-JUL-2002 (first entry)  
 XX  
 DE Phospholipase A1-related protein.  
 XX  
 KM Phospholipase A1; phospholipase inhibitor; phospholipase antagonist;  
 KM phospholipase potentiator; hypertension; cancer; blood diseases; wound.  
 XX  
 OS Unidentified.  
 XX  
 PN WO200231131-A1.  
 PD 18-APR-2002.







US-09-806-658-2  
; Sequence 2, Application US/09806658  
; Patent No. 6652851  
; GENERAL INFORMATION:  
; APPLICANT: King, Te Piao  
; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF POLISTINAE VENOM ENZYMES, S  
; FILE REFERENCE: 2313/1F138-US1  
; CURRENT APPLICATION NUMBER: US/09/806,658  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO: 2  
; LENGTH: 320  
; TYPE: PRP  
; ORGANISM: Polistes annularis  
US-09-806-658-2

Query Match 100.0%; Score 1721; DB 4; Length 320;  
Best Local Similarity 100.0%; Pred. No. 5,6e-183;  
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICLLDSTFRNGTNRGKSPDCTNEKDIVFYVSRDKRGGIILKGETLTNYDLPTKS 60  
DB 1 ICLLDSTFRNGTNRGKSPDCTNEKDIVFYVSRDKRGGIILKGETLTNYDLPTKS 60  
QY 61 TISKOVVFLHGLSTGNNENFVAMSKALIEKDPDIVISVDMKKGCNAFASRTKDALGYS 120  
DB 61 TISKOVVFLHGLSTGNNENFVAMSKALIEKDPDIVISVDMKKGCNAFASRTKDALGYS 120  
QY 121 KAVGNTRHVGFVADFTKLVEKVKYLISNIRLIGHSLGHTSGFAGKEVQKLGKYE 180  
DB 121 KAVGNTRHVGFVADFTKLVEKVKYLISNIRLIGHSLGHTSGFAGKEVQKLGKYE 180  
QY 181 IIGLDAGPYFHRSDCPDRICVTDAEYVQYIHTSIILGYVYNGSVDFYVYNGKQPGCN 240  
DB 181 IIGLDAGPYFHRSDCPDRICVTDAEYVQYIHTSIILGYVYNGSVDFYVYNGKQPGCN 240  
QY 241 EPSCSHTKAVKYLTECCKIECCIGTPWKKYFSTPKISQCRGDTVCVGLNAKSYPARG 300  
DB 241 EPSCSHTKAVKYLTECCKIECCIGTPWKKYFSTPKISQCRGDTVCVGLNAKSYPARG 300  
QY 301 AFYAPVEANAPYCHNEGKYL 320  
DB 301 AFYAPVEANAPYCHNEGKYL 320

RESULT 3  
US-08-180-209B-17  
; Sequence 17, Application US/08180209B  
; Patent No. 5593877  
; GENERAL INFORMATION:  
; APPLICANT: King, Te Piao  
; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF  
; TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND  
; TITLE OF INVENTION: HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED  
; NUMBER OF SEQUENCES: 62  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Klauder & Jackson  
; STREET: 411 Hackensack Avenue  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/180,209B  
; FILING DATE: 11-JAN-1994

CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/031,400  
; FILING DATE: 11-MAR-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 600-1-074 CIP  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201 487-5800  
; TELEFAX: 201 343-1684  
; TELEX: 133521  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 317 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-180-209B-17

Query Match 50.3%; Score 866; DB 1; Length 317;  
Best Local Similarity 54.5%; Pred. No. 1e-87;  
Matches 162; Conservative 42; Mismatches 87; Indels 6; Gaps 2;

QY 24 CTFNEKDIVFYVSRDKRGGIILKGETLTNYDLFTKSTISKOVFLHGLSTGNNENFV 83  
DB 21 CFPNSDVTVMILFTRNKRHDFTYLDTPMRHNEFKSIIRKRVFITHGFTSSATEKNFV 80  
QY 84 AMSKALIEKDPDIVISVDMKKGCNAFASRTKDALGYSKAVGNTRHVGFVADFTKLVEK 143  
DB 81 AMSKALIEKDPDIVISVDMKKGCNAFASRTKDALGYSKAVGNTRHVGFVADFTKLVEK 140  
QY 144 YKVLISNIRLIGHSLGHTSGFAGKEVQKLGKYEIIGLDAGPYFHRSDCPDRICVT 203  
DB 141 YKVLISNIRLIGHSLGHTSGFAGKEVQKLGKYEIIGLDAGPYFHRSDCPDRICVT 200  
QY 204 DAEYVQYIHTSIILGYVYNGSVDFYVYNGKQPGCN--EPSCSHTKAVKYLTECCKIE 260  
DB 201 DAHYVQIHTSSNLTGERLTGTVDFYINNQSNGPCRYIIGTCHTRAVKFTTEIIRRE 260  
QY 261 CCLIGTPWKKYFSTPKISQCRGDTVCVGLNAKSYPARGAFYAPVEANAPYCHNEG 317  
DB 261 CCLIGTPWKKYFSTPKISQCRGDTVCVGLNAKSYPARGAFYAPVEANAPYCHNEG 314

RESULT 4  
US-08-385-745-17  
; Sequence 17, Application US/08385745  
; Patent No. 5612209  
; GENERAL INFORMATION:  
; APPLICANT: King, Te Piao  
; TITLE OF INVENTION: Cloning and Recombinant Production of  
; TITLE OF INVENTION: Vespid Venom Phospholipases, and Immunological Therapies  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Penie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036-2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/385,745  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/031,400

```

: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Mirock, S. Leslie
: REGISTRATION NUMBER: 18,872
: REFERENCE/DOCKET NUMBER: 3288-020
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212 790-9090
: TELEFAX: 212 869-8864/9741
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 17:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 317 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-385-745-17

Query Match      50.3%; Score 866; DB 1; Length 317;
Beet Local Similarity 54.5%; Pred. No. 1e-87;
Matches 162; Conservative 42; Mismatches 87; Indels 6; Gaps 2;

Qy      24 CTENEKDIVFVYSSRDKRDGIILKEKTLTNYDLFTKSTISQVYFLIHGFLSTGNNEFV 83
Db      21 CPFSNDVTQMIETRENRKHDFYTLDTNRRNEFKSIKKPVFIFTHGFSATENKVF 80
Qy      84 AMSKRLIEKDFVLIVSDVKKGACNAPASTDGLGSAVANTRHVGKFAVDFTKLVEK 143
Db      81 AMSEKLMHTGFLIIMVDMRAACTDEYPGKMYEYKAVENTRLVGFIMIAKLEVQ 140
Qy      144 KYVLISNRLIGHSIGAHTSGFAGKEVOKLKGKYEKIIIGLDPAGPYFHRSDCPDRLCVT 203
Db      141 KYEPMTRIRLVGHSIGAHISGFAGKRVDELKGFSELIIGLDPAGPSPFKKNDCEKICET 200
Qy      204 DAEYVQVHTSIILGVYVNGSVDFYVYNGKNOGNCN---EPSCSHTKAVVYLTETCIKHE 260
Db      201 DAHYVQILHTSSNIGTERITGLTVDFYVYNGSNGQCRRIIGETSHTRAVVYLTETCIKRE 260
Qy      261 CCLIGTPMKKFTSPPKPIISQCRGDTCTCVGLNAKSYIPARGFVAPVEANAPYCNNG 317
Db      261 CCLIGVPSK---NPQVPSKCTRNKCVCGVGNAAKYPKRGSFYVPEAEAPYCNNG 314

RESULT 5
US-08-485-388-17
: Sequence 17, Application US/08485388
: Patent No. 6270763
: GENERAL INFORMATION:
: APPLICANT: King, Te Piao
: TITLE OF INVENTION: Cloning and Recombinant Production of
: TITLE OF INVENTION: Vaspida Venom Phospholipases, and Immunological Therapies
: NUMBER OF INVENTION: Based Thereon
: NUMBER OF SEQUENCES: 27
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Klauber & Jackson
: STREET: 411 Hackensack Avenue
: CITY: Hackensack
: STATE: New Jersey
: COUNTRY: USA
: ZIP: 07601
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/485,388
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/385,745
: FILING DATE: 08-FEB-1995
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:

```

```

1  APPLICATION NUMBER: 08/031,400
2  FILING DATE: 11-MAR-1993
3  CLASSIFICATION: 435
4  ATTORNEY/AGENT INFORMATION:
5  NAME: Jackson Esq., David A.
6  REGISTRATION NUMBER: 26,742
7  REFERENCE/DOCKET NUMBER: 600-1-074 FWCA
8  TELECOMMUNICATION INFORMATION:
9  TELEPHONE: 201 487-5800
10 TELEFAX: 201 343-1684
11
12 TELEX: 133521
13
14 INFORMATION FOR SEQ ID NO: 17:
15 SEQUENCE CHARACTERISTICS:
16 LENGTH: 317 amino acids
17 TYPE: amino acid
18 TOPOLOGY: linear
19 MOLECULE TYPE: protein
20 US-08-485-388-17
21
22 Query Match 50.3%; Score 866; DB 3; Length 317;
23 Best Local Similarity 54.5%; Pred. No. 1e-87;
24 Matches 162; Conservative 42; Mismatches 87; Indels 6; Gaps 2;
25
26 QY 24 CTRPKKQIVVYVYSRDQDGIILKKETLTYDLPSTKTSIKQVYFLHGLSTGNNPNV 83
27 | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
28 Db 21 CPFSNDVYVKNMIFLRENKRKIDFTYLDTMNHNNEFKSIIRPVFIHGFSSATEKNFV 80
29 | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
30 QY 84 AMSFALIEKODPLVYSVDWMKGACNAPASTKDALGYSKAVGNTRHVSKFVADPFLYLVEK 143
31 | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
32 Db 81 AMSFALMHTQDFLIIMDWMMACTDEYRGLKXMFYGAAGNTRLVGNFIAMLAKLVEQ 140
33 | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
34 QY 144 YKVLISNRIILGHSLGHTSGFAGKEVQKLKLGKYEIIGLDPRGPFHRSDCPDLCTV 203
35 | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
36 Db 141 YKVPMTNIRLVGHSISLGHISGFAGKRVQELDKLGFSEIIGLDPRGSPFKKIDCSERICET 200
37 | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
38 QY 204 DAEVYGVYHHSILGYYVYNGSVDFYVYNGKNQGCN--EPSSHTKAVKYLTECIKHE 260
39 | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
40 Db 201 DAHYVQLHTSSNLGTERLTGLTVDFIINCSNPGCYIITGFTCSHRAKVFTECIKRE 260
41 | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
42 QY 261 CCLIGTFWKTFFSTPKEDISQCRGDTVCVGLANKSYPARGAFYAPVEANAPYCNHG 317
43 | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
44 Db 261 CCLIGVPGSK--NPQVSKCTRNKCEVCVGLANKKYPKRGSPFYVPEAEAPYCNNG 314
45 | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
46
47 RESULT 6
48 US-08-474-853-17
49 Sequence 17, Application US/08474853
50 Patent No. 6287559
51 GENERAL INFORMATION:
52 APPLICANT: King, Te-Biao
53 TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
54 TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND
55 TITLE OF INVENTION: HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED THEREON
56 NUMBER OF SEQUENCES: 62
57 CORRESPONDENCE ADDRESS:
58 ADDRESSEE: Klauber & Jackson
59 STREET: 411 Hackensack Avenue
60 CITY: Hackensack
61 STATE: New Jersey
62 COUNTRY: USA
63 ZIP: 07601
64 COMPUTER READABLE FORM:
65 MEDIUM TYPE: Floppy disk
66 COMPUTER: IBM PC compatible
67 OPERATING SYSTEM: PC-DOS/MS-DOS
68 SOFTWARE: PatentIn Release #1.0, Version #1.25
69 CURRENT APPLICATION DATA:
70 APPLICATION NUMBER: US/08/474,853
71 FILING DATE: 07-JUN-1995
72 CLASSIFICATION: 435
73 PRIOR APPLICATION DATA:
74 APPLICATION NUMBER: US 08/180,209
75 FILING DATE: 11-JAN-1994

```

```

1 PRIOR APPLICATION DATA:
2 APPLICATION NUMBER: US 08/031,400
3 FILING DATE: 11-MAR-1993
4 ATTORNEY/AGENT INFORMATION:
5 NAME: Jackson Esq., David A.
6 REGISTRATION NUMBER: 26,742
7 REFERENCE/DOCKET NUMBER: 600-1-074 CIPB
8 TELECOMMUNICATION INFORMATION:
9 TELEPHONE: 201 487-5800
10 TELEFAX: 201 343-1684
11 TELEX: 133521
12 INFORMATION FOR SEQ ID NO: 17:
13 SEQUENCE CHARACTERISTICS:
14 LENGTH: 317 amino acids
15 TYPE: amino acid
16 TOPOLOGY: linear
17 MOLECULE TYPE: protein
18 CIS-08-474-853-17

```

Query Match	50.3%	Score 866	DB 3	Length 317
Best Local Similarity	54.5%	Pred. No. 1e-87	87	Indels 6
Matches 162	Conservative 42	Mismatches 87	Indels 6	Gaps 2

```
Qy      24 CTFNEKDIVEVYVSRRKRDGIILKETLTNYDLFTKSITSKQVLEIHGFSLSTGNNEFV 83
        | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db      21 CPFSNDVTVMITLTRENKRHDFYTLDTNNRHNKKSSIIKRPVFITHGFTSSATEKGNF 80
```

Qy 84 AMSKALIEKDFLIVSDWKKGACNAFASTKDALGYSKAVGNTRHVGKPEVADFTKLVER 1433

Db 81 AMSKALMHGTDFLIVMDWRRAACTDEYPLGLKMYFAAAGNTRLVGNFIAMIAKLVEQ 1400

```
Qy      144 YKVLISNIRPLIGHSIGAHTSGFAGKEVOKLKGKYKEIIGLDPAGPYFHRSDDPDLCTV 203
|||:::||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||:||
Db      141 YKVEMTNIRLVGHSIGAHTSFPAGRKVQELKLGFSEIIIGLDPAGPFYKANDCSERICT 200
```

QY 204 DAEEYQVHIHTSIILGVYYNNGSVDFVYNYGKQPGCN--EPSCSHKAVKYLTECTKHE 260

DB 201 DAHYVQIILHTSSNLGTERLTGTVDPIINNGSNQPGCYIIIGTCSHKRAVKYFTCELRRE 260

QY 261 CCLIGTPMKKYSTPKPISQCRGDTCVGLNAKSYPARGAFYAPVEANAPYCHNEG 317  
||| | : : : | | | | | : | | | | : |  
Db 261 CCLIGVPSQK--NPQPVSKCTRNECVGLNAKKYPRGSPFYVPEAEAPYCNNG 314

## RESULT 7

US-05-106-205B-1,  
; Sequence 17, Application US/09166205B

GENERAL INFORMATION:

;; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND HYALURONIDASE, AND IMMUNOLOGICAL, TITLE OF INVENTION: SUCH AS PHOSPHOLIPASE AND HYALURONIDASE, AND IMMUNOLOGICAL,

FILE REFERENCE: 2313/0F138US

```

; CURRENT APPLICATION NUMBER: 05/09/166,205B
; CURRENT FILING DATE: 1998-10-01

```

```

; SOFTWARE: FastSEQ for Windows Version 3.0

```

LENGTH: 317  
TYPE: DPM

ORGANISM: *Dolichovespula maculata*  
ITS-09-166-205B-17

Query Match 50.3%: Score 866: DB 3: Length 317:

Matches 162; Conservative 42; Mismatches 87; Indels 6; Gaps 2;

24 CFHNE DIVEFVYSRDKRGGILNKRETLINNDLETKSTISKQVFLHGFSLTGNNENFV 83

QY 84 AMSKALIEKDFLVISVDWKKGACNAFASTKDALGYSKAVGNTRHVGFVADFTKLVEK 143

Db 81 ANSEALMHTGDELIIIMVDRMAACTCDEYFGKIKYFFAAVGNITLVGNFLAMIAKLVEQ 140

Qy 144 YKLLISNRIILSHISGAHTSGFAGKEVOKLIGKYEIILGLDPAGPYFHRSDCPDRLCVT 203

Db 141 KYKPMNITLVGHISGAHSGFAGKGRVBLGKFSLEITGLDPAGPSPFKNDSEKICET 200

Qy 204 DAEYVIVHTSIILGVYVNVGSDVPYVYVGNQOECN---EPSCSHTKAVKYLTECIKHE 260

Db 201 DAHYVLIHTSSNLTGERTLTGVDPYIINSGNSOGCRRIIGETCSHTRAKYFTPECIRRE 260

Qy 261 CCLIGTPMKKYEFTSKPIISOGRGDTCVCGIINAKSPARGAFYAVPEANAPYCHNEG 317

Db 261 CCLIGTPGSK---NQPVSKTRBCEVCVGLNAKPIPRGSGFYVPAEAEPYCINNNG 314

RESULT 8  
US-09-806-658-7  
: Sequence 7. Application US/09806658

GENERAL INFORMATION:

; TITLE OF INVENTION: CLONING

FILE REFERENCE: 2313/1F138-US1

NUMBER OF SEC ID NOS: 13  
CURRENT FILING DATE: 2001-03-30

```

; SOFTWARE: PatenCn Version 3.0
: SEO ID NO 7

```

TYPE: PRT

US-09-806-658-7

Query Match	Score	DB 4	Length
50.38	866		317

Matches 162; Conservative 42; Mismatches 87; Indels 6; Gaps 2,

24 C I F N E K D I V F Y V S R D K R D G I L L K R E T L I N Y D L F I K S T I S K Q V F L I H G F S I G N N E N F V

21 CFFOND VAMIF DIKENNKUDE I DDIINNUNEE KND I LNF VFI I IHOE I SDAI ENNF V

[illegible]

---

[illegible]

204 DAEVVOVHTSTTIGVYVNVGSVDFVNVGKNBGCN---EPSCSHTKAVKYI.TECTKHE 260

Db 201 DAHYVOILHTSSNLGTERTLGTVDFYINNGSNOPGCRYIIGETCSHTPAVKYFTECIRRE 260

261 CCLIGTPWKYFSTPKPISQCRGDTVCVGLNAKSYPARGAFYAPVEANAPYCHNEG 317

Db 261 CCLIGVPQSK---NPQPVSKCTRNECVCVGLNAKKYPRGSFYVPVEAEAPYCNNG 314

## RESULT 9

Sequence 17, Application PC/TUS9402629  
GENERAL INFORMATION:

APPLICANT: King, Te-piao  
TITLE OF INVENTION: CLONING

TITLE OF INVENTION: HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED THEREON

CORRESPONDENCE ADDRESS:

CITY: Hackensack







Query Match	49.7%;	Score 856;	DB 5;	Length 300;
Best Local Similarity	53.2%;	Pred. No. 1.2e-86;		
Matches 159;	Conservative 51;	Mismatches 83;	Indels 6;	Gaps 2;

Qy	22	PDCSTNEMKDLVFVYVSRDRDDGIIKKELTYNDLFTSTSIKOVFLIHQFLSTGNEN	81
Db	2	KPCFPMSDVSIISIIETRENRNDLYTLQLOQNHPEPKKITTIRPVFTTHQFSSABETN	61
Qy	82	FVAMSKALIEKDDFLVISVDMKKACNAPASTYDLAGYSKAVGNTRHGKFLVADPYLLV	141
Db	62	FINAAKALVDKDMVWVISIDWQTPAACTEMAAGIKLYVPTAARNTRLVGQYIAITITKLV	121
Qy	142	EKKVKVILSNRLIGHSLGAGTSGPAGKEVQYKJLKGYEIITGLDPAGYFPRSSPCPRLC	201
Db	122	KHYKISMANIRLIGHSLGHAASGFAKKVQELIKLCKYSEIITGLDPARSPFNSNCSRLC	181
Qy	202	VTDAEYVQVLIHTSIILGVYVNVGSVDVYVNVKNOPGCN---EPGCSHTKAVKYLTECIC	258
Db	182	ETDAEYVQVLIHTSNYLGTEKTLGTVDVYMNNGKNOPGCGRPFSEVCSHRAVIYMACIC	241
Qy	259	HEDCILGTPMKKVFSPKPIISOCRBDTCVGVNLKSPARGAFAFAPVPEANA.PVCNHEG	317
Db	242	HECCLLIGIPSK---SSQPISTCTOECVGVNLAKKTKTSKSFVPEVPESTVPEPCNNKG	297

Search completed: April 27, 2005, 12:53:49  
Job time : 46 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 27, 2005, 12:53:08 ; Search time 136 Seconds

(Without alignments)  
783.038 Million cell updates/sec

Title: US-10-688-011-2

Perfect score: 1721  
Sequence: 1 ICFLLDDSTFRNGTNRGM.....AFYAPVEANAPYCHNEGIKL 320

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1424015 seqs, 332791073 residues

Total number of hits satisfying chosen parameters: 1424015

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/prodata/2/pubppaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/prodata/2/pubppaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/prodata/2/pubppaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/prodata/2/pubppaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/prodata/2/pubppaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/prodata/2/pubppaa/PCRTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/prodata/2/pubppaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/prodata/2/pubppaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/prodata/2/pubppaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/prodata/2/pubppaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/prodata/2/pubppaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/prodata/2/pubppaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/prodata/2/pubppaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/prodata/2/pubppaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/prodata/2/pubppaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/prodata/2/pubppaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/prodata/2/pubppaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/prodata/2/pubppaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/prodata/2/pubppaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/prodata/2/pubppaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1721	100.0	320	16	US-10-688-011-2
2	949.5	55.2	303	10	US-09-847-208-88
3	873.5	50.8	336	10	US-09-847-208-168
4	866	50.3	317	10	US-09-847-208-87
5	866	50.3	317	16	US-10-688-011-7
6	864	50.2	300	10	US-09-847-208-164
7	856	49.7	300	16	US-10-688-011-8
8	339	19.7	415	15	US-10-467-248-5
9	339	19.7	489	10	US-09-963-160-12
10	336	19.5	434	16	US-10-872-198-41
11	336	19.5	434	17	US-10-872-197A-41
12	327	19.0	329	14	US-10-163-547-5
13	322	18.7	451	14	US-10-163-547-3

14	322	18.7	451	14	US-10-157-031-76	Sequence 76, App1
15	322	18.7	451	14	US-10-220-380-5	Sequence 5, App1
16	322	18.7	452	15	US-10-312-088-37	Sequence 37, App1
17	311.5	18.1	353	14	US-10-128-449A-4	Sequence 4, App1
18	311.5	18.1	354	9	US-09-978-295A-178	Sequence 178, App
19	311.5	18.1	354	9	US-09-978-697-178	Sequence 178, App
20	311.5	18.1	354	9	US-09-978-192A-178	Sequence 178, App
21	311.5	18.1	354	9	US-09-999-832A-178	Sequence 178, App
22	311.5	18.1	354	10	US-09-978-189-178	Sequence 178, App
23	311.5	18.1	354	10	US-09-978-608A-178	Sequence 178, App
24	311.5	18.1	354	10	US-09-978-585A-178	Sequence 178, App
25	311.5	18.1	354	10	US-09-978-191A-178	Sequence 178, App
26	311.5	18.1	354	10	US-09-978-403A-178	Sequence 178, App
27	311.5	18.1	354	10	US-09-978-564A-178	Sequence 178, App
28	311.5	18.1	354	10	US-09-978-833A-178	Sequence 178, App
29	311.5	18.1	354	10	US-09-999-915A-178	Sequence 178, App
30	311.5	18.1	354	10	US-09-978-824-178	Sequence 178, App
31	311.5	18.1	354	10	US-09-918-585A-178	Sequence 178, App
32	311.5	18.1	354	10	US-09-999-834A-178	Sequence 178, App
33	311.5	18.1	354	10	US-09-978-423A-178	Sequence 178, App
34	311.5	18.1	354	10	US-09-978-193A-178	Sequence 178, App
35	311.5	18.1	354	10	US-09-999-830A-178	Sequence 178, App
36	311.5	18.1	354	10	US-09-978-757A-178	Sequence 178, App
37	311.5	18.1	354	10	US-09-978-187B-178	Sequence 178, App
38	311.5	18.1	354	10	US-09-978-643A-178	Sequence 178, App
39	311.5	18.1	354	10	US-09-978-375A-178	Sequence 178, App
40	311.5	18.1	354	10	US-09-978-298A-178	Sequence 178, App
41	311.5	18.1	354	10	US-09-978-188A-178	Sequence 178, App
42	311.5	18.1	354	10	US-09-978-681A-178	Sequence 178, App
43	311.5	18.1	354	10	US-09-978-194A-178	Sequence 178, App
44	311.5	18.1	354	10	US-09-999-829A-178	Sequence 178, App
45	311.5	18.1	354	10	US-09-978-299A-178	Sequence 178, App

#### ALIGNMENTS

RESULT 1  
US-10-688-011-2  
Sequence 2, Application US/10688011  
Publication No. US20040175393A1  
GENERAL INFORMATION:  
APPLICANT: King, Te Piao  
TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF POLISTINAE VENOM ENZYMES,  
TITLE OF INVENTION: SUCH AS PHOSPHOLIPASE AND HYALURONIDASE, AND IMMUNOLOGICAL  
FILE REFERENCE: 02313/100F138-US2  
CURRENT APPLICATION NUMBER: US/10/688,011  
CURRENT FILING DATE: 2003-10-17  
PRIOR APPLICATION NUMBER: US 09/806,658  
PRIOR FILING DATE: 2001-03-30  
PRIOR APPLICATION NUMBER: PCT/US99/23211  
PRIOR FILING DATE: 1999-10-01  
PRIOR APPLICATION NUMBER: US 09/166,205  
PRIOR FILING DATE: 1998-10-01  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 2  
LENGTH: 320  
TYPE: PRT  
ORGANISM: Polistes annularis  
US-10-688-011-2

Query Match 100.0%; Score 1721; DB 16; Length 320;  
Best Local Similarity 100.0%; Pred. No. 66-168;  
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ICFLLDDSTFRNGTNRGMSPDCTFRNEKDIYVYVSRDRDGIILKKETLTNYDFTKS 60  
DB 1 ICFLLDDSTFRNGTNRGMSPDCTFRNEKDIYVYVSRDRDGIILKKETLTNYDFTKS 60  
QY 61 TISKQVYFLHGLSTGNNENFVAMSKALIEKDDPIVIVDMKKGACNAPASFKDALGYS 120

Db 61 TISKQVFLIHGFLSTGNENFVAMSKALIEKDFLVISVDMKKGACNAFASTKDALGYS 120  
 ;  
 QY 121 KAVGNTRHVGKFAVDFTKLIVKRYKVLISNIRLIGHSLGHTSGPAGKEVQKILGKRYE 180  
 ;  
 Db 121 KAVGNTRHVGKFAVDFTKLIVKRYKVLISNIRLIGHSLGHTSGPAGKEVQKILGKRYE 180  
 ;  
 QY 181 IIGLDPAFPYFHRSDCPDLCTVDAEYVQVHTSIILGVYNNGVSDPYVYNGKNPGCN 240  
 ;  
 Db 181 IIGLDPAFPYFHRSDCPDLCTVDAEYVQVHTSIILGVYNNGVSDPYVYNGKNPGCN 240  
 ;  
 QY 241 EPCSHTKAVKYLTECIKHECCILGTPWKYFSTPKPISQCRDTCVGLNAKSPYARG 300  
 ;  
 Db 241 EPCSHTKAVKYLTECIKHECCILGTPWKYFSTPKPISQCRDTCVGLNAKSPYARG 300  
 ;  
 QY 301 AFYAPVEANAPYCHNEGIRKL 320  
 ;  
 Db 301 AFYAPVEANAPYCHNEGIRKL 320  
 ;

RESULT 2  
 US-09-847-208-88  
 ; Sequence 88, Application US/09847208  
 ; Publication No. US20030082190A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Saxon, Andrew  
 ; APPLICANT: Zhang, Ke  
 ; APPLICANT: Zhu, Daocheng  
 ; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF  
 ; TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES  
 ; FILE REFERENCE: UC67.002A  
 ; CURRENT APPLICATION NUMBER: US/09/847,208  
 ; CURRENT FILING DATE: 2001-05-01  
 ; NUMBER OF SEQ ID NOS: 177  
 ; SOFTWARE: FaastSeq for Windows Version 4.0  
 ; SEQ ID NO 88  
 ; LENGTH: 303  
 ; TYPE: PRT  
 ; ORGANISM: Dolichovespula maculata (White-face hornet)  
 US-09-847-208-88

Query Match 55.2%; Score 949.5; DB 10; Length 303;  
 Best Local Similarity 57.6%; Pred. No. 1e-88;  
 Matches 175; Conservative 52; Mismatches 68; Indels 9; Gaps 5;  
 QY 19 GMSPDCTFNEKDIVFYVYSRDKRDGIIKKETLTNYDLFTKSTI-SKQVFLIHGFLSG 77  
 ;  
 Db 1 GILPECKLYPBEISFVLSSTRENDGYVLTLOKLKNGMFMNSDLSKKYPLIHGFISSA 60  
 ;  
 QY 78 NNEFVAMSKALIEKDFLVISVDMKKGAC-NAFASTKDALGYSAVGNTRHVGKFAVD 136  
 ;  
 Db 61 TNKNVADMTRALLDKODIMVISTIDMRDACSNEFALLK-FIGYPAVENTRAVGKVIADF 119  
 ;  
 QY 137 TKLIVKRYKVLISNIRLIGHSLGHTSGPAGKEVQKILGKRYEIIIGLDPAFPYFHRSDC 196  
 ;  
 Db 120 SKLLQKRYKVLLENIRLIGHSLGHTSGPAGKEVQKILGKRYEIIIGLDPAFPYFHRSDC 179  
 ;  
 QY 197 PDLCTVDAEYVQVHTSIILGVYNNGVSDPYVYNGKNPGCN---EPCSHTKAVKYL 253  
 ;  
 Db 180 PERICTDAHYVQIHTSSNLGTERLTGVDFTYINSGNPGCTYIIIGETCSHTRAVKYL 239  
 ;  
 QY 254 TECIRKECCILGTPWKYFSTPKPISQCRDTCVGLNAKSPYARGAFYAPVEANAPYC 313  
 ;  
 Db 240 TECIRKECCILGTPWKYFSTPKPISQCRDTCVGLNAKSPYARGAFYAPVEANAPYC 296  
 ;  
 QY 314 HNEG 317  
 ;  
 Db 297 NNNG 300

RESULT 3  
 US-09-847-208-168  
 ; Sequence 168, Application US/09847208  
 ; Publication No. US20030082190A1

; GENERAL INFORMATION:  
 ; APPLICANT: Saxon, Andrew  
 ; APPLICANT: Zhang, Ke  
 ; APPLICANT: Zhu, Daocheng  
 ; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF  
 ; TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES  
 ; FILE REFERENCE: UC67.002A  
 ; CURRENT APPLICATION NUMBER: US/09/847,208  
 ; CURRENT FILING DATE: 2001-05-01  
 ; NUMBER OF SEQ ID NOS: 177  
 ; SOFTWARE: FaastSeq for Windows Version 4.0  
 ; SEQ ID NO 168  
 ; LENGTH: 336  
 ; TYPE: PRT  
 ; ORGANISM: Vespaula vulgaris (yellow jacket) (Wasp)  
 US-09-847-208-168

Query Match 50.8%; Score 873.5; DB 10; Length 336;  
 Best Local Similarity 52.0%; Pred. No. 7.6e-81;  
 Matches 166; Conservative 55; Mismatches 87; Indels 11; Gaps 4;  
 QY 2 CFLDDSTFRKGTLANRGSPOCTFNEKDIVFYVYSRDKRDGIIKKETLTNYDLFTKST 61  
 ;  
 Db 23 CYHGDPPLSYE--LDRG--PKCPNSDVSIIITRENRNDLYTLQTLQNHPEFKKT 77  
 ;  
 QY 62 ISKQVFLIHGFLSTGNENFVAMSKALIEKDFLVISVDMKKGACNAFASTKDALGYSK 121  
 ;  
 Db 78 ITRPVFTIHGFTSSASENFNLAKALVDKNVAVISIDMOTAACTNBAAGKILYFT 137  
 ;  
 QY 122 AVGNTRHVGKFAVDFTKLIVKRYKVLISNIRLIGHSLGHTSGPAGKEVQKILGKRYE 181  
 ;  
 Db 138 AARNTFLVQYIATITQKLVKHYKISMANIRLIGHSLGHTSGPAGKEVQKILGKRYE 197  
 ;  
 QY 182 IGLDPAFPYFHRSDCPDLCTVDAEYVQVHTSIILGVYNNGVSDPYVYNGKNPGCN- 240  
 ;  
 Db 198 IGLDPAFPYFHRSDCPDLCTVDAEYVQVHTSIILGVYNNGVSDPYVYNGKNPGCN 257  
 ;  
 QY 241 --EPCSHTKAVKYLTECIKHECCILGTPWKYFSTPKPISQCRDTCVGLNAKSPYA 298  
 ;  
 Db 258 FSEVCSHRAVITYMAECIKHECCILGTPKSK---SSQPISSCTQCEVCVGLNAKSPY 314  
 ;  
 QY 299 RGAFYAPVEANAPYCHNEG 317  
 ;  
 Db 315 RGSFYVPVESTAPFCNNKG 333

RESULT 4  
 US-09-847-208-87  
 ; Sequence 87, Application US/09847208  
 ; Publication No. US20030082190A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Saxon, Andrew  
 ; APPLICANT: Zhang, Ke  
 ; APPLICANT: Zhu, Daocheng  
 ; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF  
 ; TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES  
 ; FILE REFERENCE: UC67.002A  
 ; CURRENT APPLICATION NUMBER: US/09/847,208  
 ; CURRENT FILING DATE: 2001-05-01  
 ; NUMBER OF SEQ ID NOS: 177  
 ; SOFTWARE: FaastSeq for Windows Version 4.0  
 ; SEQ ID NO 87  
 ; LENGTH: 317  
 ; TYPE: PRT  
 ; ORGANISM: Dolichovespula maculata (White-face hornet)  
 US-09-847-208-87

Query Match 50.3%; Score 866; DB 10; Length 317;  
 Best Local Similarity 54.5%; Pred. No. 4.1e-80;  
 Matches 162; Conservative 42; Mismatches 87; Indels 6; Gaps 2;  
 QY 24 CTFNEKDIVFYVYSRDKRDGIIKKETLTNYDLFTKSTISKQVFLIHGFLSTGNENFV 83  
 ;

Db	21	CPFENDVTKMIFLTRNRKHDFTYLDPMNRNBEFKSIIKRPVVFITHGPTSSATEKNVF	80
Qy	84	AMSKALLEKODEFLVYSVDMKKGACNAPASTRKDALGYSKAVGNRHNRCKFPADFTKLLYER	143
Db	81	AMSSALMHTGDFLLIMWDMRAACTDEYPGILKTFYFAAANGNRLVGNFTAMAKLVEE	140
Qy	144	YKVLISNIRLIGHSIGSAHTSGFAGKEVOKLKGXKEIIGLDPAFPYFHRSDCPDLCTV	203
Db	141	YKVPMTNIRLGVHSLGAHISGFAGKRVQELKGFSSIIILDDPAGPSPFKKNDOSERICET	200
Qy	204	DAEYVOUIHRSIIIGVYTNVGSVDIFYNYGKNOPGCN--EPSCSHTKAVKYLTECTKHE	260
Db	201	DAHVVOILHTSSNIGTERLTGTYDIFYNMSNPGCXYIIIGECSSHTRAVKYETTECIRRE	260
Qy	261	CCILGTPMKKYFSTPKEPISOCRGDTGCVGNLNASYPARGAFYAPVANNPYCNHSG	317
Db	261	CCILIGVQSK---NPQEPVSKCTRRECYCVGLNMAKRYPKGSSFYVPEVAEAPYCNNG	314

```

RESULT 5
US-10-688-011-7
; Sequence 7, Application US/10688011
; Publication No. US20040175393A1
; GENERAL INFORMATION:
; APPLICANT: King, Te Piao
; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF POLISTINAE VENOM ENZYMES
; TITLE OF INVENTION: SUCH AS PHOSPHOLIPASE AND HYALURONIDASE, AND IMMUNOLOGICAL
; FILE OF INVENTION: THERAPIES BASED THEREON
; FILE REFERENCE: 02313/1100F138-US2
; CURRENT APPLICATION NUMBER: US/10/688, 011
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: US 09/806,658
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/US99/23211
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 09/166,205
; PRIOR FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Dolichovespula maculata
; US-10-688-011-7

```

[illegible]

RESULT 6  
US-09-847-208-164  
; Sequence 164, Application US/09847208

```

1  Publication No. US20030082190A1
2  GENERAL INFORMATION:
3
4  APPLICANT: Saxon, Andrew
5
6  APPLICANT: Zhang, Ke
7
8  APPLICANT: Zhu, Daocheng
9
10 TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
11 TITLE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
12
13 FILE REFERENCE: UC67.002A
14
15 CURRENT APPLICATION NUMBER: US/09/847,208
16
17 CURRENT FILING DATE: 2001-05-01
18
19 NUMBER OF SEQ ID NOS: 177
20
21 SOFTWARE: FastSeq for Windows Version 4.0
22
23 SEQ ID NO 164
24
25 LENGTH: 300
26
27 TYPE: PR1
28
29 ORGANISM: Vespula maculifrons (Eastern yellow jacket) (waap)
30
31 US-09-847-208-164

```

Query Match	50.2%;	Score 864;	DB 10;	Length 300;
Best Local Similarity	54.0%;	Pred. No. 6.1e-80;		
Matches	162;	Conservative	51;	Mismatches 79; Indels 8; Gaps 4;
Qy	22	PDCIFNEKQIVFYVYSDKRDGIIKKETLTNDLPFKSTISKQVVLINGIFLSTGNEN	81	
Dp	2	PKCFENSDTVSIIETRENNRDLTYLTQTLQNHHEFKKTIITRVVITIGFTSSASEK	61	
Qy	82	FVAMSKLIEKDDPLVLSVDMKGCAC--NAEASTKDALGYSKAVGNTNHQKFEVADFPLTL	140	
Dp	62	FINALKALVDKDNMVAISIDMQPAACNBEYGLKVAV-YPLAASNTRLVGQYIATITQKL	120	
Qy	141	VEKKTKVLSINRILIGHSLGAHTSGFPAKEVQKLKLGKKEITLGLDPGPFPHSDCDRL	200	
Dp	121	VKDKTISMANIRLIGHSLGAHVSGFAPKRVQELKGYSEITIGDPAFPSPDSHCSERL	180	
Qy	201	CVTDAEYVQVLIHTSIIIGVYVNVGSVDVYVNYGKNQPGC---EPSCSHKAAVYLTLECI	257	
Dp	181	CETDAEYVQVLIHTSNVLTGETKIIGTVDFVYMNNGKNNPGCRPFSEVCSTHRAIVYMAECI	240	
Qy	258	KHECCILGTFMWKCYFSTPKRISQCRGTCYCYGLNAYSAPARAGFYAPVEMNAPYCNBG	317	
Dp	241	KHECCILGIFPSRK---SSQPSIRCTKQECVCGVGNAAKYSRSGSFYVPEVSTAFPCNNKG	297	

```

RESULT 7
US-10-688-011-8
; Sequence 8, Application US/10688011
; Publication No. US20040175393A1
; GENERAL INFORMATION:
; APPLICANT: King, Te Piao
; TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF POLISTINAE VENOM ENZYMES,
; TITLE OF INVENTION: SUCH AS PHOSPHOLIPASE AND HYALURONIDASE, AND IMMUNOLOGICAL
; TITLE OF INVENTION: THERAPIES BASED THEREON
; FILE REFERENCE: 02313/100P138-US2
; CURRENT APPLICATION NUMBER: US/10/688,011
; CURRENT FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: US 09/806,658
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/US99/23211
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: US 09/166,205
; PRIOR FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 8
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Vespula vulgaris
; US-10-688-011-8

```

Query Match	49.7%	Score 856	DB 16	Length 300
Best Local Similarity	53.2%	Pred. No. 4	1e-79	
Matches 159, Conservative	51	Mismatches 83	Indels 6	Gaps 2

Qy	22	PDCSTPEKNDIVFVYVYSDRDRDGIILKKEKTELTVYDFTSTSTSKOVAFIHEFSLSTGNEN	81
Db	2	PKCFPSDVSIIIEERENRNDLYTLQTLQNHPEKKKTIITRPVFTTHEFTSSAETN	61
Qy	82	FVAMSKALIEKDDFLVIVDMWKAGCNAFSTKDALGYSKAVGNTRHYKEFVADFTKLV	141
Db	62	FINALAKALVDKDMYVMSIDMOWAFCNTENAAIGKLYLPTAARNRLTGOYIAITITOKLV	121
Qy	142	EKKYVILSNRLTGHSLGAGTSGFPAKEVOXKLKIGYKEITIGLDPAGYFHRSSCPRLC	201
Db	122	KHYKISMANRLTGHSLGAGHAGSFPAKKOQELKLGKTSIEIIGLDPARSPFSNHCSELC	181
Qy	202	VTDAEVVOVHTSIILGVYVNGSVDFVYVNGKPOGCN--EPSSHTKAVKYLTJECIK	258
Db	182	ETDAEVQOITHTSNYGTETKILGTVDVYVNNNGKPOGCRRFSEVCHSRRAVIYMAECIK	241
Qy	259	HECCILCTPMKKYFSTPKPISOCRGDTCTCVGLNKAYPAGAFAPYPEZAAFPCHNHG	317
Db	242	HECCILGIPSK--SSQPISTCTQECVCEVLNKKKTSRSFVPEVPEVPEVPCPNNGK	297

```

RESULT 8
US-10-467-248-5
Sequence 5, Application US/10467248
Publication No. US20040086905A1
GENERAL INFORMATION:
APPLICANT: DAS, Debopriya; YAO, Monique G.;
APPLICANT: ARVIZU, Chandra S.; BAUGHN, Mariah R.;
APPLICANT: LU, Yan; HAPALIA, April J.A.;
APPLICANT: CHAWLA, Narinder K.; GRUPEIN, Jennifer A.;
APPLICANT: LU, Dying Aina M.; YUE, Henry;
APPLICANT: DING, Li; ELLIOTT, Vicki S.;
APPLICANT: FORSTHEE, Ian J.; RAMKUMAR, Jayalaxmi;
APPLICANT: GANDHI, Aneena R.; TSON, Craig H.;
APPLICANT: WARREN, Bridget A.; TANG, Y. Tom;
APPLICANT: EMERLING, Brooke M.; HONCHELL, Cynthia D.;
APPLICANT: LYNE, Michael; BARROSO, Ines
TITLE OF INVENTION: LIPID-ASSOCIATED MOLECULES
FILE REFERENCE: PI-0358 USN
CURRENT APPLICATION NUMBER: US/10/467,248
CURRENT FILING DATE: 2003-08-06
PRIOR APPLICATION NUMBER: PCT/US02/03813
PRIOR FILING DATE: 2002-02-06
PRIOR APPLICATION NUMBER: US 60/266,910
PRIOR FILING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: US 60/276,891
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: US 60/276,855
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: US 60/279,760
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: US 60/283,818
PRIOR FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: US 60/285,405
PRIOR FILING DATE: 2001-04-20
NUMBER OF SEQ. ID NOS: 18
SOFTWARE: PERL Program
SEQ ID NO 5
LENGTH: 415
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: 7474074CD1
US-10-467-248-5

```

Query Match	19.7%	Score 339	DB 15	Length 415
Best Local Similarity	32.8%	Pred. No. 8.3e-26		
Matches	96	Conservative	38	Mismatches 107
				Indels 52
				Gaps 11
Qy	53	NYDLFTSKSRQVFLIHGFLSTGN---	NENFYAMSKALIEKDPFLYSIVMKKACN	108
		.....	.....	
Db	18	NNSLNVTNNTOKTKTWLLIHGYPVPSISPLMLONF---	RLILNEDNMNVIYVDSMGATTT	74
		.....	.....	

```

Qy 109 AFASITDALGYSKAAVGNRPHQKFPADDTKLLVEKYKULISNIRLISHSGHTSPAGK 168
Db 75 FL-----YNAVAKTRKVAVSLSHYIKULL-KHGASLDNHFHFIVSGASHSGVVG- 124
Qy 169 EVOKLTGLKGYKEIIGLDPAQPYFHRSDCPRLCVTDAAVYVVIHT-SIIIGVYVNVGSD 227
Db 125 ---KIFHGLGKITGIDPAGPRFSKSKPPYSLDYTDAKFVDVIVHSDNSGLGIDEPGLHID 181
Qy 228 FYVNYKQNDPGCNPE-----SCSHTKAVKLTLECKHECCILGTPMKKY--FSIPKP 277
Db 182 FYVNGGNKPPGCPKSIIFSGLIOPIKCNHORAHLPMASLETNCNFISEPCSSYNDYKT--- 238
Qy 278 ISQC-----RQDTCVCVGLNAKSY-----PARGAFYAVPAMNRYC 313
Db 239 -SLICVDDCCPFKEKSCPRISYQAKLFKVLKERMGRPLRTTVELVDISGYTPFC 290

```

```

RESULT 9
US-09-963-160-12
: Sequence 12, Application US/09963160
: Publication No. US20030165845A1
: GENERAL INFORMATION:
: APPLICANT: Kapeller-Libermann, Rosana
: APPLICANT: Chung, Myoung
: TITLE OF INVENTION: 4'6'4', A No. US20030165845A1e] Human Lipase and Uses Therefor
: FILE REFERENCE: 10147-4801
: CURRENT APPLICATION NUMBER: US/09/963.160
: CURRENT FILING DATE: 2001-09-25
: PRIOR APPLICATION NUMBER: US 60/234,915
: PRIOR FILING DATE: 2000-09-25
: NUMBER OF SEQ. ID NOS: 15
: SOFTWARE: PatentIn version 3.0
: SEQ ID NO 12
:
: LENGTH: 489
:
: TYPE: FRT
: ORGANISM: Homo sapiens
US-09-963-160-12

```

	Query Match	19.7%;	Score 339;	DB 10;	Length 489;	
	Best Local Similarity	32.8%;	Pred. No. 1e-25;			
	Matches	96;	Conservative	38;	Mismatches 107;	Indels 52; Gaps 11
Qy	53 NYDLFTKSTTSKQVFLIHGFLSTGN----	NENFVAMSKALIEKDDEFLVISDWMKKGCAN	108			
	:   :   :   :   :   :   :   :   :   :	:   :   :   :   :   :   :   :   :   :				
Dd	92 NNSLNATVPNNQKKTVMILHGYRPVGSIPMLQNFV----	RILNEDNMVIVLWDSRGATT	148			
Qy	109 AFASTKALGYSKAVNGTRHYGKRVADPTKLIVERTKYVLISNTILIGHSLCAHTSGFPAGK	168				
	:   :   :   :   :   :   :   :   :   :	:   :   :   :   :   :   :   :   :   :				
Dd	149 FI-----YNRAVKMTRKVAASLVSHIKNL-LKHGASLDNFHFIGSLAHISGFVG-	198				
Qy	169 EVOKLKLGKYEIITGLDPAGEYFRSDCPDLCTDAEAYVOVIHT-STILGVYVNVGSVD	227				
	:   :   :   :   :   :   :   :   :   :	:   :   :   :   :   :   :   :   :   :				
Dd	199 ---KIIFGQLGRITGLDPAGPREFSRKKPPYSRLDYTDKFDUVIHSDSNGLSIQEPFGHID	255				
Qy	228 FVVNYGKNOPGCENP-----SCSHTKAVKYLTETCKHECCLIQTWPKEY--FSTEXP	277				
	:   :   :   :   :   :   :   :   :   :	:   :   :   :   :   :   :   :   :   :				
Dd	256 FYPIPGAKKQGCGPCPSIFSGIQFIICNHQRAVHLPMASLETNCNIFSPFCRSYKDYKT---	312				
Qy	278 ISQC-----RGDTCVCGVLNAKSY-----PARGAFYAVEANAAYC	313				
	:   :   :   :   :   :   :   :   :   :	:   :   :   :   :   :   :   :   :   :				
Dd	313 -SLCVDCCDFEKESCPRIAGYQAKLFKGVLKERMEGRPLRTTVFLDTSGETYPEFC	364				
 RESULT 10 US-10-872-198-41 Sequence 41, Application US/10872198 Publication No. US20050002897A1 GENERAL INFORMATION: APPLICANT: Ulrich HAUPTS APPLICANT: Andre KOLTERMANN APPLICANT: Andreas SCHEIDIG APPLICANT: Christian VOBTSMEIER						



```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 329
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-163-547-5

```

```

Query Match          19.0%; Score 327; DB 14; Length 329;
Best Local Similarity 35.4%; Pred. No. 1e-24;
Matches 97; Conservative 36; Mismatches 99; Indels 42; Gaps 10;

```

```

QY 63 SKQVFLIHGFLSTGNNEFVA--MSKAL--IEKDFLIVISVDKKGA--CNAFASTDALG 118
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 45 SRKTRFLIHGFTGSEESWLSKMKRALFQVEKSGVNIYVDWLGAITBEYA--LKXIF 102
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 119 YSAVNGTRHVGKVFADFTLLVEKYKVLISNRLIGHSGANTSGPAGKEVQ---KLKL 175
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 103 YPQAVLNVRVAGAEIALQLQLEELNVSPEVNLIGHSGAHVAGAAGRFRGKTGHKL 162
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 176 GKYEKIIIGLDPAGPYFHRSDCPRLCTVDAEYVYIHT-----SIILGVYNNVGSVDF 228
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 163 GR---ITGLDPAGPYFPGTEELTRLDGDAEPVDAIHTDPSPIGPGMGKTSQRVGHVDR 219
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 229 YNAYGKN-QPGCNE-----PSCSHTKAVKYLTECIKHECCLIQTPW 268
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 220 YPAGSGSEQPGCQKIYLAQIRATRGIEWEPASVRCGHERSVKCYADSLINEYKNDGPG 279
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 269 KKXFTPKPISQCRGDTCCVCGGLNAKSYPARGAF 302
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 280 SRAVMCISYDAFLBGLCLCN--KKCPMGSY 310
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

## RESULT 13

```

US-10-163-547-3
; Sequence 3, Application US/10163547
; Publication No. US2003037350A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Glucksmann, Maria A.
; APPLICANT: Myers, Rachel
; APPLICANT: Rudolf-Owen, Laura A.
; TITLE OF INVENTION: No. US2003037350A1el nucleic acid sequences encoding a
; TITLE OF INVENTION: human ubiquitin protease, lipase, dynamin, short chain
; TITLE OF INVENTION: dehydrogenase, and ADAM-TS Metalloprotease and uses
; FILE REFERENCE: 35800/247836(5800-243)
; CURRENT APPLICATION NUMBER: US/10/163,547
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: 09/407,356
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 09/704,918
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: 09/435,311
; PRIOR FILING DATE: 1999-11-05
; PRIOR APPLICATION NUMBER: 09/796,100
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/185,503
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: 09/781,598
; PRIOR FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/182,009
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/782,952
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: 60/182,408
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/496,005
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 451
; TYPE: PRT

```

```

; ORGANISM: Homo sapiens
US-10-163-547-3

```

```

Query Match          18.7%; Score 322; DB 14; Length 451;
Best Local Similarity 30.8%; Pred. No. 5.2e-24;
Matches 92; Conservative 51; Mismatches 112; Indels 44; Gaps 13;

```

```

QY 44 IILKKEITL-----NYDLFTKSTISKOVFLIHGFLSTGNNEFV--AMSKALIEKDFLV 97
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 44 MLYTRKNLCAQTINSSAFGNLNVTKTFTFVHGFRPTSSPPVMMDDLVKGLLSVDMNV 103
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 98 ISVDMKKGACNAPASTKDALGYSKAVGNTRHVGKVFADFTLLVEKYKVLISNRLIGH 156
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 104 VVVDNMNRGA-----TLLIYTHASSKTRKVMYLKEPIDIQMLAE--GASLDDIYMIQV 153
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 157 SIGAHTSGFAGKEVOQLKIGYKEIIGLDPAGPYFHRSDCPRLCTVDAEYVYIHTSI- 215
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 154 SIGAHTSGFVG--EMVDGWLGR---ITGLDPAGPLFNGKPHQDRLPDSDAQFVDVHSDTD 209
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 216 ILGVYNNVGSVDFPYVYVNGKNQPGCNEP-----SCSHTKAVKYLTECIKHECCLIQTP 267
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 210 ALGYKEPLNIDFYFPGGLDQRCPTILIGRFQYFCKHQRVSRYLLSSLRESCTITAYP 269
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 268 WKXY--FSTPKPIS--QCRGDTCCVCG-----LNKASYPARGAFYAPVANAAYC 313
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 270 CDSYQDYRNGKCVSCGTSQKESCPLILGYVADNMWKHRLRGKDPMTKAFPDTAE--ESPFC 327
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

## RESULT 14

```

US-10-157-031-76
; Sequence 76, Application US/10157031
; Publication No. US20030108890A1
; GENERAL INFORMATION:
; APPLICANT: Baranova, A. V.
; APPLICANT: Yankovsky, N. K.
; APPLICANT: Kozlov, A. P.
; APPLICANT: Lobashev, A. V.
; APPLICANT: Kulkovskaya, L. L.
; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequences
; FILE REFERENCE: 2760-103
; CURRENT APPLICATION NUMBER: US/10/157,031
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-157-031-76

```

```

Query Match          18.7%; Score 322; DB 14; Length 451;
Best Local Similarity 30.8%; Pred. No. 5.2e-24;
Matches 92; Conservative 51; Mismatches 112; Indels 44; Gaps 13;

```

```

QY 44 IILKKEITL-----NYDLFTKSTISKOVFLIHGFLSTGNNEFV--AMSKALIEKDFLV 97
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 44 MLYTRKNLCAQTINSSAFGNLNVTKTFTFVHGFRPTSSPPVMMDDLVKGLLSVDMNV 103
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 98 ISVDMKKGACNAPASTKDALGYSKAVGNTRHVGKVFADFTLLVEKYKVLISNRLIGH 156
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 104 VVVDNMNRGA-----TLLIYTHASSKTRKVMYLKEPIDIQMLAE--GASLDDIYMIQV 153
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 157 SIGAHTSGFAGKEVOQLKIGYKEIIGLDPAGPYFHRSDCPRLCTVDAEYVYIHTSI- 215
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 154 SIGAHTSGFVG--EMVDGWLGR---ITGLDPAGPLFNGKPHQDRLPDSDAQFVDVHSDTD 209
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 216 ILGVYNNVGSVDFPYVYVNGKNQPGCNEP-----SCSHTKAVKYLTECIKHECCLIQTP 267
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 210 ALGYKEPLNIDFYFPGGLDQRCPTILIGRFQYFCKHQRVSRYLLSSLRESCTITAYP 269
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 268 WKXY--FSTPKPIS--QCRGDTCCVCG-----LNKASYPARGAFYAPVANAAYC 313
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 270 CDSYQDYRNGKCVSCGTSQKESCPLILGYVADNMWKHRLRGKDPMTKAFPDTAE--ESPFC 327
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```
RESULT 15
US-10-220-380-5
; Sequence 5, Application US/10220380
; Publication No. US20030113846A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: LAL, Preeti
; APPLICANT: YAO, Monique G.
; APPLICANT: YUE, Henry
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: TANG, Y. Tom
; APPLICANT: KHAN, Farrah A.
; APPLICANT: NGUYEN, Daniel B.
; APPLICANT: DAS, Debopriya
; APPLICANT: HILLMAN, Jennifer L.
; APPLICANT: WALIA, Narinder K.
; APPLICANT: HARALIA, April
; APPLICANT: TRIBOULEY, Catherine M.
; TITLE OF INVENTION: LIPID METABOLISM ENZYMES
; FILE REFERENCE: PI-0050 PCT
; CURRENT APPLICATION NUMBER: US/10/220,380
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 60/186,480; 60/190,415; 60/198,437
; PRIOR FILING DATE: 2000-03-02; 2000-03-17; 2000-04-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
; SEQ ID NO 5
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030113846A1 5027764CD1
US-10-220-380-5

Query Match      18.7%; Score 322; DB 14; Length 451;
Best Local Similarity 30.8%; Pred. No. 5.2e-24;
Matches 92; Conservative 51; Mismatches 112; Indels 44; Gaps 13;

Qy      44  ILKKERTL-----NYDLFTKSTISKQVPLIHGFLSTGNNEFV-AMSKALIEKDDFLV 97
Db      44  MLYTRKVLTCQQTINSSAFGNLNVTKKTFIVHGFRPTGSPVWMDLVKGLSEVDNIV 103

Qy      98  ISVDMKKGACNAFASTKDALGYSAVGNTRHVGKFAVDF-TKLIVKKYKVLISNIRLIGH 156
Db      104  VVVDMMNGA-----TTLITYHASSKTRKRVAMVLFKFDQMLAE--GASLDIYMGIV 153

Qy      157  SLGAHTSGFAGKEVOKLKIGYKEIIGLDPAQPYFHRSDCPDRLCVTDAEYVOYIHTSI- 215
Db      154  SLGAHISGFVG-EMWDGMLGR---ITGLDPAQPLFNGKPHQDRLDPSDAQFVDVHSDTD 209

Qy      216  ILGYVYVVGSDVDFVYVNGKQOPGNEP-----SCSHKAVKYLTECIKHBCCLIGTP 267
Db      210  ALGKKEPLGNIDFYPNGGLDQPGCPKTIIGGFQYFKCDHORSVYLYLSSLSRESCITAYP 269

Qy      268  WKKY--FSTPKPIS--OCRGDTCVVG-----LNKSYPARGAFYAPVEANAPYC 313
Db      270  CDSYQDYRNKGKVCSCGTSQKSCPLDGYADNMKDHLRGKDPFWTKAFPTDAE-ESPFC 327
```

Search completed: April 27, 2005, 13:06:04  
Job time : 138 secs

**THIS PAGE LEFT BLANK**



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 27, 2005, 12:44:47 ; Search time 40 Seconds  
(without alignments)  
769,734 Million cell updates/sec

Title: US-10-688-011-2

Perfect score: 1721

Sequence: 1 ICLPLDDSTFRNGTLNRGM.....AFYAPVEANAPYCHNEGIRL 320

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0 %  
Maximum Match 100 %

Listing first 45 summaries

Database :

1: PIR 79: \*  
2: PIR1: \*  
3: PIR2: \*  
4: PIR3: \*  
5: PIR4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	949.5	55.2	303	2 A44563	phospholipase A1 (
2	866	50.3	317	2 S32406	phospholipase A1 (
3	864	50.2	300	2 A44564	phospholipase A1 (
4	336	19.5	434	1 A49488	triacylglycerol 11
5	321	18.7	449	1 LIPG	triacylglycerol 11
6	312.5	18.2	461	2 S21223	triacylglycerol 11
7	309	18.0	465	2 C43357	triacylglycerol 11
8	307.5	17.9	474	1 A40570	lipoprotein lipase
9	307.5	17.9	474	1 JH0790	lipoprotein lipase
10	306.5	17.8	470	2 A54232	lipase, CoPL-RP2 -
11	305.5	17.8	475	1 LIHL	lipoprotein lipase
12	305.5	17.8	475	2 JG4242	lipoprotein lipase
13	304.5	17.7	450	1 A27053	lipoprotein lipase
14	304.5	17.7	478	2 S29846	lipoprotein lipase
15	302.5	17.6	465	1 A27330	lipoprotein lipase
16	297.5	17.3	467	2 A43357	pancreatic lipase
17	297.5	17.3	478	2 S18158	lipoprotein lipase
18	296	17.2	482	1 A46596	triacylglycerol 11
19	293.5	17.1	469	2 B43357	pancreatic lipase
20	292.5	17.0	457	2 I48206	triacylglycerol 11
21	292	17.0	490	1 S04331	lipoprotein lipase
22	290.5	16.9	482	1 A34671	triacylglycerol 11
23	289.5	16.8	465	2 S41084	triacylglycerol 11
24	288.5	16.8	473	2 S20612	triacylglycerol 11
25	287.5	16.7	467	1 LIDG	triacylglycerol 11
26	279	16.2	499	2 A28997	triacylglycerol 11
27	273.5	15.9	465	1 JG1318	triacylglycerol 11
28	268	15.6	510	2 S15893	triacylglycerol 11
29	257	14.9	494	2 A27442	triacylglycerol 11

30	167	9.7	439	1 VJPF1	vitellogenin I pre
31	154	8.9	437	2 S22889	vitellogenin I - M
32	153	8.9	356	2 S49011	yolk protein 2 - b
33	134.5	7.8	420	2 A25876	vitellogenin II p
34	129	7.5	422	2 S49012	yolk protein 3 - b
35	128	7.4	442	1 VJPF2	vitellogenin II pr
36	125.5	7.3	172	2 A45558	triacylglycerol 11
37	124	7.2	422	2 S22888	vitellogenin 2 - M
38	102	5.9	851	2 A59284	unconventional myo
39	100.5	5.8	601	2 T34396	hypothetical prote
40	100	5.8	540	2 G96716	hypothetical prote
41	98	5.7	400	2 S46814	ribosomal protein
42	97.5	5.7	494	2 T05302	vacuolar processin
43	96.5	5.6	261	2 S69709	hypothetical prote
44	96.5	5.6	909	2 T33749	hypothetical prote
45	96	5.6	261	1 F70390	probable phosphoes

#### ALIGNMENTS

##### RESULT 1

A44563

phospholipase A1 (EC 3.1.1.32), allergen Dol m 1.02 - bald-faced hornet

C/Species: Vespaula maculata (bald-faced hornet)

C/Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #ext\_change 09-Jul-2004

C/Accession: A44563

R/Hoffman, D.R.

submitted to the Protein Sequence Database, February 1994

A/Reference number: A44563

A/Accession: A44563

A/Molecule type: protein

A/Residues: 1-303 <HOF>

A/Cross-references: UNIPROT:P53357

A/Note: 55-Glu was also found; 295-Tyr was also found

C/Superfamily: triacylglycerol lipase

C/Keywords: carboxylic ester hydrolase

Query Match 55.2%; Score 949.5; DB 2; Length 303;  
Best local Similarity 57.6%; Pred. No. 1.2e-69;  
Matches 175; Conservative 52; Mismatches 68; Indels 9; Gaps 5;

QY	19	GMSPDCTFNEKDIIVFYVSRDKDGIILKKEITLTVNDLPFKSTI-SKQVFLHGLSTG	77
DB	1	GIPLBECKLVPEBISFLSTRENDRGYLTLOKLNKMKFNKNSDLSKQVFLHGFISSA	60
QY	78	NNENFVAMSKALIEKDFIVISVDMKKGAC-NAFASTXALGSKAVGNTBHYGKFAVDF	136
DB	61	TKNGVADMTBALDKDDIVISIDMDGACSNFALLK-FIGYPAVENTRAVGKTIADF	119
QY	137	TKLVEKRYKVLISNIRLISHSIGAHTSGFAGKEVQKLKQKYEIIIGLDPAGBYPFRSDC	196
DB	120	SKLIIQKVKYLENIRLIGSLGDAQAFAGKEQFQFKLGKYPEIIGLDPAGSPFKKDC	179
QY	197	PDLCTVDAEYQVIVHTSIILGYVNVGSDVFNVGKQPGCN---EESCSITKAVKYL	253
DB	180	PERICETDAHYVOIILTTSSNLGTERLGTVDYFINDGSNQPGCTYIIGTSHTRAVKYL	239
QY	254	TECIRKHECCILGPMWKYESTPPIBQCRGDTVCVGLNAKSPARGAFAPVEANAPYC	313
DB	240	TECIRRECCILIGVPSK---NPQVSKCTRNBCVCGLNAKEYPKKGSFYVPEALAPFC	296
QY	314	HNEG 317	
DB	297	NNNG 300	

##### RESULT 2

S32406

phospholipase A1 - bald-faced hornet (fragment)

C/Species: Vespaula maculata (bald-faced hornet)

C/Date: 02-Dec-1993 #sequence\_revision 26-May-1995 #ext\_change 09-Jul-2004

C/Accession: S32406



A:Experimental source: pancreas  
R.Guidoni, A.; Bonicel, J.; Bianchetto, J.; Rovey, M.  
Biochimie 61, 841-845, 1979

A>Title: Porcine pancreatic lipase. Sequence between the 235th and 307th amino acids.

A:Reference number: A90675; PMID:8008446; PMID:518929

A:Accession: A90675

A:Molecule type: protein

A:Residues: 235-307 <GUR>

A:Experimental source: pancreas

A>Note: This sequence has since been revised at positions 302 and 305

R.Benkouka, F.; Guidoni, A.A.; De Caro, J.D.; Bonicel, J.J.; Desnuelle, P.A.; Rovey, M.  
Eur. J. Biochem. 128, 331-341, 1982

A>Title: Porcine pancreatic lipase. The disulfide bridges and the sulphydryl groups.

A:Reference number: A91124; PMID:83103095; PMID:7151781

A:Contents: disulfide bonds

A:Accession: A91124

A:Molecule type: Protein

A:Residues: 1-182, E, 184-449 <BEN>

A:Experimental source: pancreas

R.Guidoni, A.; Benkouka, F.; De Caro, J.; Rovey, M.  
Biochim. Biophys. Acta 660, 148-150, 1981

A>Title: Characterization of the serine reacting with diethyl p-nitrophenyl phosphate in C.Keywords: carboxylic ester hydrolase; glycoprotein; lipid digestion  
F.4-10, 237-261, 285-296, 299-304, 433-449/Disulfide bonds: #status experimental  
P.166/Binding site: carbohydrate bonds: (or 90-103) #status experimental  
P.166/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match      18.7%; Score 321; DB 1; Length 449;  
Best Local Similarity 28.4%; Pred. No. 2.3e-18;  
Matches 88; Conservative 50; Mismatches 122; Indels 50; Gaps 8;

OY MSPDCFNEDVIVYYVSROKRDG---IIKKETLTNTDLPFKSTISQOVFLHGFLEST 76  
DB LPDP--KQVDTRRLTYTNOQNKNYQLVLADPSITT--SNFRDKRTRFPIHFIDK 80  
          ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
OY GNNEVFAMSKALIEKDPLVISDWKKAGACNAFASTDALGSXAVGNTRGVKQVADF 136  
DB GEEDWLNICKNLFKVESVNCICVDMKGSS-----RTGYQSQRIRLVGAEMAF 131  
          |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
OY 137 TKLVEKYKLISNRILIGSLGHTSGFAKEVOGLKLGKYEITGLDPAGPYFHSDC 196  
DB 132 VEYLKESLSGPSNVHVIGHSLGSHAAGEAGRFTN----GTERTTGDLPAEPFCQTGE 187  
          ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
OY 197 PDLCCTDAAYVQVIHT-----SIIIGVVYNQSVDFYNNVGKQPCNE----- 241  
DB 188 LVRLDSDAKFVNDIHTDDAIPINLGFMGQMOTVGHDLFFPGFGKMPPCCQNIITSQIWD 247  
          ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
OY 242 -----PSCSHTKAVNYLTECTIGHECCLLGTPMKKY-FSTPKPISGRGDPVCV 289  
DB 248 IDGIWEGRTPFVACNHLRISKITYYADSIIINPDGFAFPDSDYVFWANKCFPSPSECPOM 307  
          |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|:  
OY 290 GLNAKSYPAR 299  
DB 308 GHYADRPFGR 317

RESULT 6

S21223  
ctriacylglycerol lipase (EC 3.1.1.3) precursor, pancreatic - horse (fragment)  
C.Species: Equus caballus (domestic horse)  
C.Date: 22-Nov-1993 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004  
C.Accession: S21223 | S21251  
R.Kerfellec, B.; Foglitzo, E.; Bonicel, J.; Bougis, P.E.; Chapuis, C.  
Eur. J. Biochem. 206, 279-287, 1992

A>Title: Sequence of horse pancreatic lipase as determined by protein and cDNA sequencing  
A:Accession: S21223  
A.Molecule type: mRNA  
A.Residues: 1-461 <KER>

A:Cross-references: UNIPROT:P29183; EMBL:X66218; NID:g1063;PIDN:CAA6961.1; PID:g1064  
A:Molecule type: protein  
A:Accession: S21251

A:Residues: 13-78/80/97-218;220-228;230-277;322-349;384-438;440-448;450-461 <KEN>  
C:Superfamily: triacylglycerol lipase  
C:Keywords: carboxylic ester hydrolase  
F1-12/Domains: signal sequence (fragment) #status predicted <SIG>  
F13-461/Product: triacylglycerol lipase #status experimental <MAT>

Query Match 18.2%; Score 312.5; DB 2; Length 461;  
Best Local Similarity 29.0%; Pred. No. 1,1e-17;  
Matches 86; Conservative 41; Mismatches 123; Indels 47; Gaps 7;

QY 33 FVYVSADKRDG---ILKETLTNYDLFTYSTISKQVFLIHGFSTGNNEPFAVMSKL 89  
| :  
DB 51 PLLTYNENDNFQEIYADPSSTIOSNENPT-----GRKRFFIIHGFIDKEESWLSITMCQM 106  
| :  
QY 90 IEKDDELIVSYVMKKACANAFASTKALGYSKAVGNTRHVKGPAADFRLTKVEKYVLIS 149  
| :  
DB 107 FYVESVNCICVDMKSSRRTA-----YSASQNVRIVAEEVAAYLVGLDSSFDSFPS 157  
| :  
QY 150 NTRLIGSHGAHTSGFGAKEVQRLKLGKYKEIIGLDAPGFPHRSDCPDRLCVTDAEYVO 209  
| :  
DB 158 NVHIIGHSGSHAGAGARRTN----GAVGRITGLDPAEPFOGPELVLRIDSPDAQFPD 213  
| :  
QY 210 VHTSIIT-----LCVVYNVGSVDPVYNYGKNQPGCNE-----PS 243  
| :  
DB 214 VIHTDIAPFIPIMLGFQMSGTAGHLDFPPNGCKEMPCQKNTLSQIVDIDGIQGTRDFNA 273  
| :  
QY 244 GSHTAAVKTLTECIKHKECCLIQTPMKKYFS-TPRPIQCNGDTVCVCGLNKASYPAR 299  
| :  
DB 274 CNHLRSKRYTTSILNPDPGAFGSCASYSDFTANKCFPCSSEGPCMGHYADRFPCR 330  
| :

RESULT 7  
CA3357

triacylglycerol lipase (EC 3.1.1.3) precursor, pancreatic - human  
N:Alternate names: fatty acid ethyl ester synthase; pancreatic lipase  
C:Species: Homo sapiens (man)  
C:Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text change 09-Jul-2004  
C:Accession: CA3357; A34494; S08272; A60135; S34578; A34574  
R:Giller, T.; Buchwald, P.; Blum-Kaelin, D.; Hunziker, W.  
J. Biol. Chem. 267, 16509-16516, 1992

A>Title: Two novel human pancreatic lipase related proteins, hPLRP1 and hPLRP2. Differenc.  
A:Reference number: A43357; MWID:92355622; PMID:1379598  
A:Accession: CA3357

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: mRNA

A:Residues: 1-465 <GL>

A:Cross-references: UNIPROT:P16233; GB:M93285; NID:G190139; PIDN:AAA60129.1; PID:g190140  
R:Lowe, M.E.; Rosenblum, J.L.; Straus, A.W.  
J. Biol. Chem. 264, 20042-20048, 1989

A>Title: Cloning and characterization of human pancreatic lipase cDNA.  
A:Reference number: A34494; MWID:90062115; PMID:2479644  
A:Accession: A34494

A:Molecule type: mRNA

A:Residues: 1-465 <LOW>

A:Cross-references: GB:J05125; NID:g339596; PIDN:AAA36740.1; PID:g339597  
R:Winkler, F.K.; D'Arcy, A.; Hunziker, W.  
Nature 343, 771-774, 1990

A>Title: Structure of human pancreatic lipase.  
A:Reference number: S08272; MWID:90158821; PMID:2106079  
A:Accession: S08272

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 17-46/48-465 <WIN>

A>Note: part of this sequence, including the amino end of the mature protein, was confir.  
R:de Caro, A.; Bonicelli, U.; Pieroni, G.; Guy, O.  
Biochimie 63, 799-801, 1981

A>Title: Comparative studies of human and porcine pancreatic lipases: N-terminal sequen.  
A:Reference number: A60135; MWID:82069208; PMID:7306587  
A:Accession: A60135

A:Molecule type: protein





A:Residues: 182, 'N', 184-189 <MA3>  
A:Cross-references: GB:S76076; NID:g242989; PIDN:AA821000.1; PID:g242990  
A>Note: sequence extracted from NCBI backbone (NCBIN:76076, NCBIP:76129)  
A>Note: these mutations were identified in patients with LDL deficiency  
R:DiChex, H.L.; Fojo, S.S.; Beg, O.U.; Skarlatos, S.I.; Brunzelli, J.D.; Cutler Jr., G.B.  
J. Biol. Chem. 266, 473-477, 1991  
A>Title: Identification of two separate allelic mutations in the lipoprotein lipase gene  
A:Reference number: A39044; MUID:91093167; PMID:1702428  
A:Accession: A39044  
A:Molecule type: mRNA  
A:Residues: 219-223,268-272 <DIC>  
A>Note: normal sequence is shown; alleles with mutations of 221-Ile to Thr or of 270-Arg  
to His.  
Biochim. Biophys. Acta 1049, 21-26, 1990  
A>Title: Structure and polymorphic map of human lipoprotein lipase gene.  
A:Reference number: S10575; MUID:90291024; PMID:1972631  
A:Accession: S10575  
A:Molecule type: DNA  
A:Residues: 1-5,26-34,79-88,139, 'D', 141-148,177-185,255-263,336-344,376-384,437-445,472-  
A:Cross-references: GB:X52978; GB:X53518; NID:g34386  
A>Note: this translation is not annotated in Genbank entry HSLIPASE, release 114.0  
R:Rienback, S.; Ohlsson, B.G.; Samuelsson, L.; Bjursell, G.  
Mol. Cell. Biol. 12, 4622-4633, 1992  
A>Title: Characterization of the human lipoprotein lipase (LPL) promoter: evidence of two  
pl. gene during adipogenesis.  
A:Reference number: I37996; MUID:93024407; PMID:1406652  
A:Accession: I37996  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-5 <ENE>  
A:Cross-references: EMBL:X6811; NID:g34389; PIDN:CAA48230.1; PID:g4379028  
R:Goroda, T.; Yamada, N.; Kawamura, M.; Kozaki, K.; Mori, N.; Ishibashi, S.; Shimano, H.  
J. Clin. Invest. 88, 1856-1864, 1991  
A>Title: Heterogeneous mutations in the human lipoprotein lipase gene in patients with F  
A:Reference number: I55564; MUID:92091492; PMID:1752947  
A:Accession: I55564  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 228-230, 'E', 232-233 <GOT1>  
A:Cross-references: GB:S71706; NID:g240930; PIDN:AA820664.1; PID:g240931  
A:Accession: I70232  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 268-269, 'H', 271-273 <GOT2>  
A:Cross-references: GB:S71710; NID:g240928; PIDN:AA820663.1; PID:g240929  
R:Takegi, A.; Ikeda, Y.; Tsubumi, Z.; Shoji, T.; Yamamoto, A.  
J. Clin. Invest. 89, 581-591, 1992  
A>Title: Molecular studies on primary lipoprotein lipase (LPL) deficiency. One base dele  
A:Reference number: I55573; MUID:92148877; PMID:1737848  
A:Accession: I55573  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 246-247, 'LSA' <TAK2>  
A:Cross-references: GB:S81339; NID:g245360; PIDN:AA821420.1; PID:g245361  
A>Note: mutant sequence from patients with primary lipoprotein lipase deficiency  
C:Comment: The primary function of this lipase is the hydrolysis of triglycerides of cir  
protein C-II on the luminal surface of vascular endothelium, where it is anchored by a m  
C:Genetics:  
A:Gene: GDB:LPL; LIPD  
A:Cross-references: GDB:120700; OMIM:238600  
A:Map position: 8p22-8p22  
A:Introns: 380/2; 441/2  
C:Complex: homodimer  
C:Function:  
A:Description: catalyzes the hydrolysis of triacylglycerol to diacylglycerol plus a fat  
A:Pathway: lipid degradation  
C:Superfamily: triacylglycerol lipase  
C:Keywords: carboxylic ester hydrolase; glycoprotein; lipid degradation; plasma  
F.1-27/Domain: signal sequence #status predicted <SIG>  
F.128-475/Product: lipoprotein lipase #status predicted <MPT>  
F.152-169/Region: lipid binding #status predicted  
F.154-67,243-266,291-310,302-305,445-465/Disulfide bonds: #status predicted  
F.770,386/Binding site: carbohydrate (Asn) (covalent) #status predicted

```

F:159,183,268/Active site: Ser. Asp, His #status predicted

Query Match      17.8%; Score 305.5; DB 1; Length 475;
Best Local Similarity 30.3%; Pred. No. 4,4e-17;
Matches 86; Conservative 36; Mismatches 111; Indels 51; Gaps 8;

QY      63 SKQVFLIHPLSTGNNENFVAMSKLIEK--DDELIVSYDWKKGKCNFAFSTKDLGYS 120
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DQ      72 SSKETFWIHGTVTGMYESWPKLVAALYKREPSNVIVDMLSRAOE-----HYR 122
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      121 KAVENTHHVKKFVADFTKTLVEKAYKVLISNIRLIGHSIGHTSGFAGKEVOKLGYKE 180
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DQ      123 VSAGYTLTVQGDVARF INMKEEBEENPLDVLVHLGLGYSIGAHAAAGINSLTNK----KVN 178
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      181 IIGLDPAGPYFHNSDCDRLCVTDAEVYQIHT-----SIILGVYVNGSVDPFYVNGK 234
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DQ      179 ITGLDPPAGPNFEVYEAAPSRLSPDDADVDVLIHTFTPRSPPRSIGIQKPVGHVIDIYPNGGT 238
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      235 NQPCN-----EPGCSITKAVKYLITELCIHCECLIGPWWKYESTPK 276
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DQ      239 FQPCNCNGEAIKRVIAERGLGDVDQLVKCSHERSIHFLFDLSLNE---ENPSKAYRCSSK 294
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      277 PISQ-----CRGDTGVCGINKSKSVAR--GAFYAPVEANADPY 312
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DQ      295 EAFKGLCLSCRRKRCNNLGEYINKKPAKASSKMYLTKNSQMFY 338
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 12
JC4242
lipoprotein lipase (EC 3.1.1.34) precursor - baboon
C|Species: Papio sp. (baboon)
C|Date: 12-Oct-1995 #sequence _revision 08-Feb-1996 #text_change 18-Jun-1999
C|Accession: JC4242
R|Cole, S.A.; Hixson, J.E.
Gene 161, 265-269, 1995
A|Title: Baboon lipoprotein lipase: cDNA sequence and variable tissue-specific expressic
A|Reference number: JC4242; MUID:95394368; PMID:7665091
A|Molecule type: mRNA
A|Residues: 1-475 <COL>
A|Cross-references: GB-U18091; NID:G602295; PIDN:AAC50199.1; PID:G602296
C|Comment: This enzyme plays a fundamental role in lipid metabolism by catalyzing the hy
C|Genetics:
A|Gene: lpl
C|Superfamily: triacylglycerol lipase
C|Keywords: carboxylic ester hydrolase; glycoprotein; lipoprotein
F:1-37/Domain: signal sequence #status predicted <SIG>
F:28-475/Product: lipoprotein lipase #status predicted <AM>
F:70-386/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:159,183,268/Active site: Ser, Asp, His #status predicted

Query Match          17.8%; Score 305.5; DB 2; Length 475;
Best local similarity 30.3%; Pred. No. 4,4e-17;
Matches    86; Conservative   36; Mismatches 111; Indels   51; Gaps      8;

QY      63 SKQVFLIHGLSTGNENFVMSKALIEK--DPLIVISVMKKAGCNAPASTDALGYS 120
DB      72 SSKTFMVIHGWTVTGVMESEWPELVVALYKRBPDSNVIVDWLSRA-----QQHY P 122
QY      121 KAVGTRHVGRKVADFTKLIVEKYKVLINIRLIGSLGHNTSGFAKEYOKLTGKYKE 180
DB      123 VSAGTKLVGGDVAFIFNMWEEEFNYPLDNVHLGLSLGHAAGIASLTLNK---KNR 178
QY      181 IIGDPAGPYFHRSOCPDLCTVDAEYVOYIHT-----SIILGYVYNNGSVDFVYNYGK 234
DB      179 ITGLDPAGPNFYAEAPSLSPDDADFVDYLHFTFGSPERSIGIQKPVGHVIDIYPNGGT 238
QY      235 NOPGCN-----EESCSHTKAAKYLTECIKHCCILGPWKYFYSTPK 276
DB      239 FPGGNGIGAIVIAERGLGDVDQLVKCSHERSIIHFIDLNE----ENPSKA YRCSSK 294
QY      277 PISQ-----CGDTTCVCGLNAKSYPAR--GAIFYAPEANAPY 312

```







GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 27, 2005, 12:35:36 ; Search time 176 Seconds

(without alignments)  
931.053 Million cell updates/sec

Title: US-10-688-011-2

Perfect score: 1721  
Sequence: 1 ICFLLDDSTFRNGTINRGM.....AFYAPVEANAPYCHNESIKL 320

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : UnIProt 03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1619	94.1	301	1	PAL POLAN
2	1444	83.9	337	2	O6Q252
3	1442	83.8	316	2	O6Q250
4	1437	83.5	316	2	O6Q249
5	1437	83.5	316	2	O6Q251
6	949.5	55.2	303	1	PAL2 DOLMA
7	873.5	50.8	336	1	PAL1 VESVU
8	866	50.3	317	1	PAL1 DOLMA
9	864	50.2	300	1	PAL1 VESMC
10	357.5	20.8	472	2	O6P221
11	357.5	20.8	472	2	O642T5
12	353.5	20.5	346	2	O68KKO
13	347.5	20.2	460	2	O6P223
14	345	20.0	576	2	O7Q8Y5
15	342.5	19.9	676	2	O9VB94
16	340.5	19.8	852	2	O7P217
17	340	19.8	347	2	O66KK1
18	339	19.7	347	2	O7SZ70
19	339	19.7	481	2	O6XZB0
20	338.5	19.7	472	2	O642R3
21	336	19.5	434	2	P81139
22	333.5	19.4	428	2	O7Q259
23	329	19.1	284	2	O7ZYK0
24	327	19.0	452	2	O9BDJ4
25	325.5	18.9	481	2	O6P658
26	323.5	18.8	540	2	O9W448
27	322	18.7	451	2	O6MW18
28	322	18.7	525	2	O7QEV4
29	321.5	18.7	451	2	O8CIV3
30	318.5	18.5	450	1	LIPF PIG
31	316.5	18.4	277	2	O7QA39

32	315.5	18.3	449	2	O8BXB5	O8bxb5 mus musculu
33	314.5	18.3	456	2	O6NYZ4	O6nyz4 brachydanio
34	314.5	18.3	465	2	O6P8U6	O6p8u6 mus musculu
35	313.5	18.2	305	2	O7P215	O7p215 anopheles g
36	312.5	18.2	461	1	LIPF HORSE	P29183 equus caball
37	311.5	18.1	339	2	O9VB50	O9vb50 drosophila
38	311.5	18.1	354	2	O6UW82	O6uw82 homo sapien
39	311.5	18.1	350	2	O6ZUS9	O6zus9 homo sapien
40	310.5	18.0	460	2	O641F6	O641f6 xenopus lae
41	310.5	18.0	500	1	LIPF HUMAN	O9y5x9 homo sapien
42	310.5	18.0	500	2	O6P9C8	O6p9c8 homo sapien
43	310.5	18.0	1000	2	O9VX01	O9vx01 drosophila
44	310	18.0	341	2	O9VB88	O9vb88 drosophila
45	309.5	18.0	475	1	LIPF MUSVI	O46647 mustela vis

## ALIGNMENTS

RESULT 1  
PAL POLAN STANDARD; PRT; 301 AA.  
ID OSU6M0;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Phospholipase A1 (EC 3.1.1.32) (EC 3.1.1.4) (Allergen Pol a 1).  
OS Pholistes annularis (Paper wasp).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
OC Vespidae; Polistinae; Polistes.  
OX NCBI\_TaxID=27505;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA King T.P., Lu G.;  
RL Submitted (JUG-1999) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: Hydrolysis of phosphatidylcholine with phospholipase A2 (EC 3.1.1.4) and phospholipase A1 (EC 3.1.1.32) activities (By similarity).  
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-acylglycerophosphocholine + a carboxylate.  
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 2-acylglycerophosphocholine + a carboxylate.  
CC -!- SUBUNIT: Monomer.  
CC -!- ALLERGEN: Causes an allergic reaction in human.  
CC -!- SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase family.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See [http://www.isb-sib.ch/announce/](http://www.isb-sib.ch/announce/or send an email to license@sib-sib.ch) or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC -----  
DR EMBL; AF174527; AAD52615.1; -.  
DR HSSP; P16233; 1GPL.  
DR InterPro; IPR002334; DOL/Ves\_allerg.  
DR InterPro; IPR000734; Lipase\_AS.  
DR InterPro; IPR008263; Lipase\_AS.  
DR InterPro; IPR000379; Ser\_estrs.  
DR Pfam; PF00151; Lipase; 1.  
DR PRINTS; PR00821; TAGLIPASB.  
DR PROSITE; PS00120; LIPASE\_SER; 1.  
KW Allergen; Hydrolase; Lipid degradation.  
FT ACT\_SITE 138 Charge relay system (By similarity).  
FT ACT\_SITE 166 Charge relay system (By similarity).  
SQ SSOURCE 301 AA; 33483 MW; 6A0B7DC76FDC047 CRC64;  
Query Match 94.1%; Score 1619; DB 1; Length 301;  
Best Local Similarity 100.0%; Pred. No. 7.7e-125;  
Matches 301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 20 MSPDCTFENEKDI VEVYVYSRDKRDGII LKKEITLNTYDLFTKSTISKOVFLIHGFLSTGNN 79
    |||||
DB 1 MSBDCITFNEKDI VEVYVYSRDKRDGII LKKEITLNTYDLFTKSTISKOVFLIHGFLSTGNN 60
    |||||
QY 80 ENFVMSKALIEKDEFLVISVDMWKGACNAFASTKDALGYSKAVGNTRHVGKVFADFTKL 139
    |||||
DB 61 ENFVMSKALIEKDEFLVISVDMWKGACNAFASTKDALGYSKAVGNTRHVGKVFADFTKL 120
    |||||
QY 140 LVEKYVVLISNIRLIGHSLGAHTSGFAGKEVOUKLIGKYKEIIGLDPAGYFHRSDCPDR 199
    |||||
DB 121 LVEKYVVLISNIRLIGHSLGAHTSGFAGKEVOUKLIGKYKEIIGLDPAGYFHRSDCPDR 180
    |||||
QY 200 LCVTDAEYVOVITSTIILGVYVNGSVDFVYVNGKNOGCGNEPSCSHTKAVKLTCEICIH 259
    |||||
DB 181 LCVTDAEYVOVITSTIILGVYVNGSVDFVYVNGKNOGCGNEPSCSHTKAVKLTCEICIH 240
    |||||
QY 260 ECLLIGTPWKKYFSTPKPISQCRGDTCCVGLNAKSYPARGAFYAVEANAPYCHNEGIG 319
    |||||
DB 241 ECLLIGTPWKKYFSTPKPISQCRGDTCCVGLNAKSYPARGAFYAVEANAPYCHNEGIG 300
    |||||
QY 320 L 320
    |||||
DB 301 L 301
    |||||
```

## RESULT 2

```
Q6Q252 PRELIMINARY; PRT; 337 AA.
ID 06Q252
AC 06Q252;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
OS Venom phospholipase A1 precursor.
OC Polistes dominulus (European paper wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Polistinae; Polistes.
OX NCBI_TaxId=34728;
RN [1]
RP SEQUENCE FROM N.A.
RA Moawad T.I.S., Hoffman D.R.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY566645; AAS67043.1; -.
DR GO; GO:0003824; F: catalytic activity; IEA.
DR GO; GO:0008970; F: phospholipase A1 activity; IEA.
DR GO; GO:0006629; P: lipid metabolism; IEA.
DR InterPro; IPR002334; DoI/Ves_allerg.
DR InterPro; IPR000734; Lipase.
DR InterPro; IPR008262; Lipase_AS.
DR InterPro; IPR000379; Ser_estrs.
DR Pfam; PF00151; Lipase_1.
DR PRINTS; PRO0825; DOLALLERGEN.
DR PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
KW SIGNAL.
FT SIGNAL 1 21 Potential.
FT CHAIN 36 337 venom phospholipase A1 1.
SQ SEQUENCE 337 AA; 37559 MW; C0A7E0E5EBDE448C CRC64;
```

Query Match 83.9%; Score 1444; DB 2; Length 337;  
Best Local Similarity 83.1%; Pred. No. 2.1e-110;  
Matches 265; Conservative 24; Mismatches 30; Indels 0; Gaps 0;

```
QY 2 CFFLDSTFRNCTLRGMSPDCTFNEKDI VEVYVYSRDKRDGII LKKEITLNTYDLFTKSTISK 61
    |||||
DB 19 CIAADULTLRNCTLRGTPDCTFNEKDI ELHVSYRDKRNGIILKKEITLKNYDLFOKQISHQ 78
    |||||
QY 62 ISKQVFLIHGFLSTGNNENFVMSKALIEKDEFLVISVDMWKGACNAFASTKDALGYSK 121
    |||||
DB 79 ISHQVILIHGFLSTGNNENFVMSKALIEKDEFLVISVDMWKGACNAFASTKDALGYSK 138
    |||||
QY 122 AVGNTRHVGKVFADFTKLVEKYVVLISNIRLIGHSLGAHTSGFAGKEVOUKLIGKYKEI 181
    |||||
```

```
DB 139 AVGNTRHVGKVFADFTKLVEKYVVMNSNIRLIGHSLGAHTSGFAGKEVOUKLIGKYKEI 198
    |||||
QY 182 IGLDPAGYFHRSDCPDRLCVTDAEYVOVITSTIILGVYVNGSVDFVYVNGKNOGCGNE 241
    |||||
DB 199 IGLDPAGYFHRSDCPDRLCVTDAEYVOVITSTIILGVYVNGSVDFVYVNGKNOGCGNE 258
    |||||
QY 242 PSCSHTKAVKLTCEICIKHECCILGTPWKKYFSTPKPISQCRGDTCCVGLNAKSYPARG 301
    |||||
DB 259 PSCSHTKAVKLTCEICIKHECCILGTPWKKYFSTPKPISQCRGDTCCVGLNAKSYPARG 318
    |||||
QY 302 FYAVPEANAPYCHNEGIGKL 320
    |||||
DB 319 FYAVPEANAPYCHNEGIGKL 337
    |||||
```

## RESULT 3

```
Q6Q250 PRELIMINARY; PRT; 316 AA.
ID 06Q250
AC 06Q250;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
OS Venom phospholipase A1 3 (Fragment).
OC Polistes dominulus (European paper wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Polistinae; Polistes.
OX NCBI_TaxId=34728;
RN [1]
RP SEQUENCE FROM N.A.
RA Moawad T.I.S., Hoffman D.R.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY566647; AAS67043.1; -.
DR GO; GO:0003824; F: catalytic activity; IEA.
DR GO; GO:0008970; F: phospholipase A1 activity; IEA.
DR GO; GO:0006629; P: lipid metabolism; IEA.
DR InterPro; IPR002334; DoI/Ves_allerg.
DR InterPro; IPR000734; Lipase.
DR InterPro; IPR008262; Lipase_AS.
DR InterPro; IPR000379; Ser_estrs.
DR Pfam; PF00151; Lipase_1.
DR PRINTS; PRO0825; DOLALLERGEN.
DR PROSITE; PS00120; LIPASE_SER; UNKNOWN_1.
FT NON TER 1 1
FT CHAIN 14 >316 venom phospholipase A1 3.
FT NON TER 316 316
SQ SEQUENCE 316 AA; 35019 MW; 12CB3A7748F8FE05 CRC64;
```

Query Match 83.8%; Score 1442; DB 2; Length 316;  
Best Local Similarity 84.4%; Pred. No. 2.9e-110;  
Matches 266; Conservative 21; Mismatches 28; Indels 0; Gaps 0;

```
QY 6 DDSTFRNCTLRGMSPDCTFNEKDI VEVYVYSRDKRDGII LKKEITLNTYDLFTKSTISKQ 65
    |||||
DB 2 DDLTTLRNCTLRGTPDCTFNEKDI ELHVSYRDKRNGIILKKEITLKNYDLFOKQISHQ 61
    |||||
QY 66 VVFLIHGFLSTGNNENFVMSKALIEKDEFLVISVDMWKGACNAFASTKDALGYSKAVGN 125
    |||||
DB 62 IAILIHGFLSTGNNENFVMSKALIEKDEFLVISVDMWKGACNAFASTKDALGYSKAVGN 121
    |||||
QY 126 TRHVGKVFADFTKLVEKYVVLISNIRLIGHSLGAHTSGFAGKEVOUKLIGKYKEIIGD 185
    |||||
DB 122 TRHVGKVFADFTKLVEKYVVMNSNIRLIGHSLGAHTSGFAGKEVOUKLIGKYKEIIGD 181
    |||||
QY 186 PAGYFHRSDCPDRLCVTDAEYVOVITSTIILGVYVNGSVDFVYVNGKNOGCGNEPSCS 245
    |||||
DB 182 PAGYFHRSDCPDRLCVTDAEYVOVITSTIILGVYVNGSVDFVYVNGKNOGCGNEPSCS 241
    |||||
QY 246 HTKAVKLTCEICIKHECCILGTPWKKYFSTPKPISQCRGDTCCVGLNAKSYPARGAFYAP 305
    |||||
DB 242 HTKAVKLTCEICIKHECCILGTPWKKYFSTPKPISQCRGDTCCVGLNAKSYPARGAFYAP 301
    |||||
QY 306 VEANAPYCHNEGIGKL 320
    |||||
```

RESULT 6			
PA12_DOLMA			
ID_PA12_DOLMA	STANDARD;	PRT;	303 AA.
AC	P53357;		
DT	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	25-OCT-2004 (Rel. 45, Last annotation update)		
DE	Phospholipase A1 2 (EC 3.1.1.32) (EC 3.1.1.4) (Allergen Dol m 1.02)		
DE	Dol m 1.)		
OS	Dolichovespula maculata (White-face hornet) (Bald-faced hornet).		
OS	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; A1		
OC	Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea		
OC	Vespidae; Vespinae; Dolichovespula.		
OX	NCBI_TaxId=7441;		
RN	[1]		
RN	SEQUENCE.		
RP	TISSUE=Venom;		
RC	MEDLINE=94257972; PubMed=8199462;		

RA Hoffman D.R.;  
RT "Allergens in hymenoptera venom. XXVI: the complete amino acid  
RL sequences of two vespid venom phospholipases.";  
CC Int. Arch. Allergy Immunol. 104:184-190(1994).  
CC - FUNCTION: Hydrolysis of phosphatidylcholine with phospholipase A2  
CC (EC 3.1.1.4) and phospholipase A1 (EC 3.1.1.32) activities.  
CC - CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-  
CC acylglycerophosphocholine + a carboxylate.  
CC - CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 2-  
CC acylglycerophosphocholine + a carboxylate.  
CC - ALLELGEN: Causes an allergic reaction in human.  
CC - SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase  
CC family.  
CC PIR: A44563; A44563.  
DR HSSP: P54318; 1BU8.  
DR InterPro: IPR002334; DoI/Ves\_allerg.  
DR InterPro: IPR000734; Lipase.  
DR InterPro: IPR008262; Lipase\_AS.  
DR InterPro: IPR000379; Ser\_estrs.  
DR Pfam: PF00151; Lipase; 1.  
DR PRINTS: PR00821; TAGLIPASE.  
DR PROSITE: PS00120; LIPASE\_SER; 1.  
KW Allergen; Direct protein sequencing; Hydrolase; Lipid degradation;  
KW Multigene family.  
KW ACT\_SITE 140 140 Charge relay system (By similarity).  
FT ACT\_SITE 168 168 Charge relay system (By similarity).  
FT VARIANT 55 55 G -> E.  
FT VARIANT 295 295 F -> Y.  
SQ SEQUENCE 303 AA; 33782 MW; 85816A837C0F3AF8 CRC64;  
  
Query Match 55.2%; Score 949.5; DB 1; Length 303;  
Best Local Similarity 57.6%; Pred. No. 8.4e-70;  
Matches 175; Conservative 52; Mismatches 68; Indels 9; Gaps 5;  
  
QY 19 GMSPDCTFNEKDIIVFYVYSRDKDGIILKKEITLTYDLFTKSTI-SKQVFLIHGLSLTG 77  
DB 1 GILPECKLVPEEISFVLSTRENDGVYLTQLKNGKMFNQSLSKKVPFLIHGPISSA 60  
QY 78 NNFNFAMSKALIEKDPFLIVSVWKKKAC-NAFASTKALGVSKVGNTRHVGKRVADP 136  
DB 61 TNKNVADMTKALDKODIMVTSIDMRDAGCSNEFALIK-FTGPKAVENRAVGTATADP 119  
QY 137 TKLVKKYKVLISNIRLIGSLGAHTSGFAGKEVQKIKLGKYEIIIGLDPAGPYFHRSDC 196  
DB 120 SKTLQKYKVLINIRLIGHSLGAQIAGFAGKEFGQFKIGKYEIIIGLDPAGSPFKKDC 179  
QY 197 PDLCTDAEYVQVYIHTSIILGVYVNVGSDVFTVYNGKQPGCN---EPSCSTKAVKYL 253  
DB 180 PERICETDAHYVQIHTSSNLGTERLTGVDVFINDSNPGCTYIIGETCSHTRAVKYL 239  
QY 254 TETIKHECCLIIGPMKKYFSTPKPIISQCRGDTCCVGLNAKSYPARGAFAFYAEANAPYC 313  
DB 240 TETIRRECCLIIGVPSK---NPQPVSKCTRNCECVGLNAKEIFPKGSPFIVEALQAPFC 296  
QY 314 HNEG 317  
DB 297 NNNNG 300  
  
RESULT 7  
PAL\_VESVU  
PAL\_PAL\_VESVU STANDARD; PRT; 336 AA.  
AC P49369;  
DT 01-FEB-1996 (Rel. 33, Created)  
DT 01-FEB-1996 (Rel. 33, Last sequence update)  
DT 25-OCT-2004 (Rel. 43, Last annotation update)  
DE Phospholipase A1 precursor (EC 3.1.1.32) (EC 3.1.1.4) (Allergen Ves v  
1) (Ves v 1).  
OS Vespa vulgaris (Yellow jacket) (Wasps).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
OC Vespidae; Vespinae; Vespa.  
OX NCBI\_TaxID=7454;

RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 37-65; 165-183; 247-263 AND  
RX 273-294  
RA MEDLINE=96426243; PubMed=8828537;  
RA King T.P., Lu G., Gonzalez M., Qian N., Solatova L.;  
RT "Yellow jacket venom allergens, hyaluronidase and phospholipase:  
RT sequence similarity and antigenic cross-reactivity with their hornet  
RT and wasp homologs and possible implications for clinical allergy.";  
RL J. Allergy Clin. Immunol. 98:588-600(1996).  
CC - FUNCTION: Hydrolysis of phosphatidylcholine with phospholipase A2  
CC (EC 3.1.1.4) and phospholipase A1 (EC 3.1.1.32) activities (By  
CC similarity).  
CC - CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-  
CC acylglycerophosphocholine + a carboxylate.  
CC - CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 2-  
CC acylglycerophosphocholine + a carboxylate.  
CC - ALLELGEN: Causes an allergic reaction in human.  
CC - SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase  
CC family.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: L43561; AAB48072.1; -.  
DR HSSP: PL6233; ILPB.  
DR InterPro: IPR002334; DoI/Ves\_allerg.  
DR InterPro: IPR000734; Lipase.  
DR InterPro: IPR008262; Lipase\_AS.  
DR InterPro: IPR000379; Ser\_estrs.  
DR Pfam: PF00151; Lipase; 1.  
DR PROSITE: PS00120; LIPASE\_SER; 1.  
KW Allergen; Direct protein sequencing; Hydrolase; Lipid degradation;  
KW Signal.  
FT SIGNAL 1 36  
FT CHAIN 37 336 Phospholipase A1.  
FT ACT\_SITE 173 173 Charge relay system (By similarity).  
FT ACT\_SITE 201 201 Charge relay system (By similarity).  
FT CONFLICT 37 37 G -> F (in Ref. 1; AA sequence).  
SQ SEQUENCE 336 AA; 37676 MW; 65548B7F5B56456 CRC64;  
  
Query Match 50.8%; Score 873.5; DB 1; Length 336;  
Best Local Similarity 52.0%; Pred. No. 1.7e-63;  
Matches 166; Conservative 55; Mismatches 87; Indels 11; Gaps 4;  
  
QY 2 CFLDSTTFNRAGTLNRGMSPDCTFNEKDIIVFYVYSRDKDGIILKKEITLTYDLFTKST 61  
DB 23 CYGHDDPLSYE---LDRG--PKCPNSDPTVSIIETRENRNDLTTLQTLQNHPRFKKTI 77  
QY 62 ISKQVFLIHGLSLGNNENFVAMSKALIEKDPFLIVSVWKKKACNAPASTKDALGYSK 121  
DB 78 ITRPVFITHGFTSSASETNFINLAKALVDKDNVYVTSIDWQTACTAEAGLKYLYPT 137  
QY 122 AVGNTRHVGKFAADFTKLIVKKYKVLISNIRLIGSLGAHTSGFAGKEVQKIKLGKYEI 181  
DB 138 AARNRRLVGQYIATYQKLVKHYKISMANTIRLIGHSLGAHAGFGAKVQDELKGYSTI 197  
QY 182 IGLDPAGPYFHRSDCPDRLCTVDAEYVQIHTSIILGVYVNVGSDVFTVYNGKQPGCN- 240  
DB 198 IGLDAPRPSFSDNRKSERICETDAHYVQIHTSSNLGTERLTGVDVFINNKNKQPGCOR 257  
QY 241 --EPSCSTKAVKAVYLTECIKHECCLIIGPMKKYFSTPKPIISQCRGDTCCVGLNAKSYPA 298  
DB 258 FSEVSHBRAVIYMAECIKHECCLIIGIPSK---SSQPISSCTKQECVGLNAKPKYS 314  
QY 299 RGAFAPVYANAPYCHNEG 317  
DB 315 RGSFVYVEASTAPFCNNKG 333

```

RESULT 8
PAIL_DOLMA
ID_PAIL_DOLMA STANDARD; PRT; 317 AA.
AC Q06478;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Phospholipase A1 precursor (EC 3.1.1.32) (EC 3.1.1.4) (Allergen Dol
m 1.01) (Dol m 1) (Fragment).
OS Dolichovespula maculata (White-face hornet) (Bald-faced hornet).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Dolichovespula.
OX NCBI_TaxID=7441;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=93209375; PubMed=8458431; DOI=10.1016/0014-5793(93)80080-E;
RA Soldatova L., Kochoumian L., King T.P.;
RT "Sequence similarity of a hornet (D. maculata) venom allergen
phospholipase A1 with mammalian lipases."
RL FEBS Lett. 320:145-149(1993).
CC -1- FUNCTION: Hydrolysis of phosphatidylcholine with phospholipase A2
(CC (EC 3.1.1.4) and phospholipase A1 (EC 3.1.1.32) activities.
CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC acylglycerophosphocholine + a carboxylate.
CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 2-
CC acylglycerophosphocholine + a carboxylate.
CC -1- ALLERGEN: Causes an allergic reaction in human.
CC -1- SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase
CC family.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
CC EMBL; X66869; CAA47341.1; -.
DR PIR; S32406; S32406.
DR HSSP; P54318; 1B08.
DR InterPro; IPR002334; Dol/Ves_allerg.
DR InterPro; IPR000734; Lipase.
DR InterPro; IPR008262; Lipase_AS.
DR InterPro; IPR000379; Ser_estrs.
DR Pfam; PF00151; Lipase; 1.
DR PROSITE; PS00120; LIPASE_SER; 1.
KW Allergen; Direct protein sequencing; Glycoprotein; Hydrolase;
KW Lipid degradation; Multigene family; Signal.
FT SIGNAL 1 17
FT NON_TER 1 1
FT CHAIN 18 317 Phospholipase A1.1.
FT ACT_SITE 154 154 Charge relay system (By similarity).
FT ACT_SITE 182 182 Charge relay system (By similarity).
FT CARBOHYD 25 25 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 229 229 N-linked (GlcNAc...) (Potential).
FT VARIANT 271 271 N->S.
SQ SEQUENCE 317 AA; 35708 MW; 0B2135FD45312D9 CRC64;

Query Match 50.3%; Score 866; DB 1; Length 317;
Best Local Similarity 54.5%; Pred. No. 6; Se-63;
Matches 162; Conservative 42; Mismatches 87; Indels 6; Gaps 2;

QY CTFNEKQIVFYVSRDGRDGIILKKTITVNDLFTKSTIKOVFLIHGFLSTNNENFV 83
DB 21 CFPNSNDVYKMTFLTRKRDFTYLDVNRNRFKSIIRKPVFTFGFTSSATEKNFV 80
QY AMSKALKLEKDFLVISVDMKKGACNAPASTKDALGYSKAVGNTRHVGKFFVADFTKLLVER 143
DB 81 AMSBALMHTGDFLLIIVDMMAACTDEYPLGKVMFYKAAVGNTRLVGNFLAMLAKKLVQ 140

```

```

RESULT 9
PAIL_VESMC
ID_PAIL_VESMC STANDARD; PRT; 300 AA.
AC P51528;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Phospholipase A1 (EC 3.1.1.32) (EC 3.1.1.4) (Allergen Ves m 1) (Ves m
DE 1).
OS Vespula maculifrons (Eastern yellow jacket) (Wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespula.
OX NCBI_TaxID=7453;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=94257972; PubMed=8199462;
RA Hoffman D.R.;
RT "Allergens in hymenoptera venom. XXVI: the complete amino acid
RT sequences of two vespid venom phospholipases."
RL Int. Arch. Allergy Immunol. 104:184-190(1994).
CC -1- FUNCTION: Hydrolysis of phosphatidylcholine with phospholipase A2
(CC (EC 3.1.1.4) and phospholipase A1 (EC 3.1.1.32) activities (By
CC similarity).
CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC acylglycerophosphocholine + a carboxylate.
CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 2-
CC acylglycerophosphocholine + a carboxylate.
CC -1- SUBUNIT: Monomer.
CC -1- ALLERGEN: Causes an allergic reaction in human.
CC -1- SIMILARITY: Belongs to the AB hydrolase superfamily. Lipase
CC family.
CC PIR; A44564; A44564.
DR HSSP; P00591; 1ETH.
DR InterPro; IPR002334; Dol/Ves_allerg.
DR InterPro; IPR000734; Lipase.
DR InterPro; IPR008262; Lipase_AS.
DR InterPro; IPR000379; Ser_estrs.
DR Pfam; PF00151; Lipase; 1.
DR PRINTS; PR00821; TNGLIPASE.
DR PROSITE; PS00120; LIPASE_SER; 1.
KW Allergen; Direct protein sequencing; Hydrolase; Lipid degradation.
KW Allergen; Direct protein sequencing; Hydrolase; Lipid degradation.
FT ACT_SITE 137 137 Charge relay system (By similarity).
FT ACT_SITE 165 165 Charge relay system (By similarity).
FT VARIANT 97 97 A->M.
FT VARIANT 191 191 I->P.
FT VARIANT 202 202 I->L.
SQ SEQUENCE 300 AA; 33540 MW; 8E2DE20BD69CCF6 CRC64;

Query Match 50.2%; Score 864; DB 1; Length 300;
Best Local Similarity 54.0%; Pred. No. 8; Se-63;
Matches 162; Conservative 51; Mismatches 79; Indels 8; Gaps 4;

QY PDCFNEKQIVFYVSRDGRDGIILKKTITVNDLFTKSTIKOVFLIHGFLSTNNENFV 81
DB 2 PKCFNSNDVYKMTFLTRKRDFTYLDVNRNRFKSIIRKPVFTFGFTSSATEKNFV 80
QY FVMSKALKLEKDFLVISVDMKKGACNAPASTKDALGYSKAVGNTRHVGKFFVADFTKLL 140

```

```

Db      62  FILALALVDKXMYWISIDMQAACNREBPGKAVY-VPTASNRRLVQVIATITTKL 120
      141  VEKXKVLISNRIIGSLGHTSGFAGKEVQKILGKYKEITGLDPAGPYFHRSDCPDL 200
      121  VKDYKISMANIRILIGHSIGLGHVSGFAGKRVQELKGLGYSEIIGIDPARPFSDNHCSERL 180
Qy      201  CVTDAEVQVYTHSIILGVYVNWGVDFYVNGKNPGCN---EPSCSHTKAVKYLTECI 257
      181  CETDAEYVQIIRHSNLTIGTKIIGVDFINNGKNKPGCCRFSEVCSHRAVIYIABCI 240
Db      258  KHECCILGTPWKYFTSPKPIEQCRGDTVCVGLNKSYPARGAFYAPVEANAPYCHNEG 317
      241  KHECCILGTPRSK---SSQGISRCTQKQECVGLNKKYPSRGSFYVPEVSTAPFCNNGK 297

RESULT 10
Q6P221  PRELIMINARY; PRT; 472 AA.
ID      1  O6P221
AC      1  O6P221;
DT      05-JUL-2004 (TrEMBLrel. 27, Created)
DT      05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT      05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE      Hypothetical protein MGC76224.
GN      Name=MGC76224;
OS      Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC      Xenopodidae; Xenopus.
OX      NCBI_TaxID=8364;
RN      1
RP      SEQUENCE FROM N.A.
RC      TISSUE=Embryo;
RX      MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Ueudin T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA      Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA      Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
RA      Jones S.J., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN      12
RP      SEQUENCE FROM N.A.
RC      TISSUE=Embryo;
RX      Klein S., Gerhard D.S.;
RA      Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC      -1- SIMILARITY: Contains 1 Pfam domain.
EMBL: BC064243; AAH64243.1; -
DR      GO: GO:0003824; F:catalytic activity; IEA.
DR      GO: GO:0004806; F:triacylglycerol lipase activity; IEA.
DR      GO: GO:0006629; P:lipid metabolism; IEA.
DR      InterPro: IPR000773; Lipase.
DR      InterPro: IPR008262; Lipase_AS.
DR      InterPro: IPR002331; Lipase_panc.
DR      InterPro: IPR001024; Lipoxigenase_LH2.
DR      InterPro: IPR008976; Pfam_LH2.
DR      InterPro: IPR000379; Ser_gstrs.
DR      Pfam: PF00151; Lipase; 1.
DR      Pfam: PF01477; Pfam; 1.
DR      PRINTS: PR00823; PANCILIPASE.

```

```

DR      PRINTS: PR00821; TAGLIPASE.
DR      SMART: SM00308; LH2; 1.
DR      PROSITE: PS00120; LIPASE_SER; 1.
KW      Hypothetical protein.
SQ      SEQUENCE 472 AA; 51948 MW; 3B5407A2BBA9A6D6 CRC64;
      Query Match 20.8%; Score 357.5; DB 2; Length 472;
      Best local Similarity 31.0%; Pred. No. 6.5e-21;
      Matches 91; Conservative 43; Mismatches 109; Indels 51; Gaps 7;

Qy      50  TLTNIDLFYKSTISKQVFLIHGFLSTGNENFVAMSKALIKDPLVIVDMKGCACNA 109
      79  SLTFNFTSKRSR-----FIHGFIDGEGENLVNMCKAMLEVEDNCPCTMSSGSRIT 132
Db      110  PASTDIALGYSKAVGNTRHVGFVDFDTLVEKXKVLISNRIIGHSIGHTSGPAGKE 169
      133  -----YTDANNIRVGAELAFIYGLSSKMKYPLSNVHIIGHSIGSTHAGEVGR 183
Qy      170  VKKLKGLKYKEIIGLDPAGPYFHRSDCPDLCTVDAEVQVYHT-----SILGVYNN 222
      184  MGEL-----GRITGLDPAGPYFQNTPIEVRLDPTAVFVDAIHTDPLIPMGYGMGQS 238
Qy      223  VGSVDFFYVYGNKQPCNEP-----SCGHTAAVKYLTCIKHCECL 263
      239  VAHMDFFPNGCHRMPCGSKPIIAKLIDIDGLWEGSKDIPACNHLRSYKXTYESISPDGF 298
Qy      264  IGPWKYKYSTPKPIS-QCRGDTVCVGLNKSYPARG---AFYAPVEANAPY 312
      299  VGPTSTYEAFTKGTGFCPTTGCPLMGHYADAFSSHGTSIDSYFLNLTSGKPY 352

RESULT 11
Q642T5  PRELIMINARY; PRT; 472 AA.
ID      1  Q642T5
AC      1  Q642T5;
DT      25-OCT-2004 (TrEMBLrel. 28, Created)
DT      25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT      25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE      Hypothetical protein.
OS      Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC      Xenopodidae; Xenopus.
OX      NCBI_TaxID=8364;
RN      1
RP      SEQUENCE FROM N.A.
RC      TISSUE=Embryo;
RX      PubMed=12477932; DOI=10.1073/pnas.242603899;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Ueudin T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,
RA      Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA      Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
RA      Jones S.J., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length human
RT      and mouse cDNA sequences";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN      12
RP      SEQUENCE FROM N.A.
RC      TISSUE=Embryo;
RX      Klein S., Gerhard D.S.;
RA      Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.

```

DR EMBL: BC080957; AA080957.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 472 AA; 51908 MW; 490157A2BBA9B666 CRC64;

Query Match 20.8%; Score 357.5; DB 2; Length 472;  
 Best Local Similarity 31.0%; Pred. No. 6.5e-21;  
 Matches 91; Conservative 43; Mismatches 109; Indels 51; Gaps 7;

QY 50 TLTVYDPTKSTISKQVFLHGLSTGNNENFVAMS KALIEKDFLVISVDMKKACNA 109  
 DB SLTFNFKTSRKS-----FIHGFIDSGEENMLVMCKAMKVEDVNCFCFDMGGSGRTI 132  
 QY 110 FASTKDALGYSKAVGNTRHVCKPVAADFVKLIVEKYKULISIRLIGHSLGHTGSPAGKE 169  
 DB 133 -----YTQANNNIRVGAELAYFTIGYISSMKTPLSVNHLIGHSLGHTGSEVGR 183  
 QY 170 VOKLKLGKYEIIIGLDPAQPFYHRSDCPDRLCVTDAEYVQVHT-----SILGYVYN 222  
 DB 184 MPGI-----GRITGLDPAGPFQNTPIEVRLDPTDAFVDALHTDTPDLIPKMGYMSQS 238  
 QY 223 VGSYDFVYVNGKQOPGCEP-----SCSHTKAVKYLTECIKHECCL 263  
 DB 239 VAHNDFFPNGGEMNPGCSKPLAKLIDIGLMEGSKDIFACNHLRSYKYTESISSPDGF 298  
 QY 264 IGFPMKKYFSPPKIS-QCRGDTVCVGLNAKSPARG----AFYAVENAPY 312  
 DB 299 VGPISTSYEAFPTKGTGFPCTTGCPLMGHYADAFSSHQSDSYFLNTGSEKPY 352

## RESULT 12

068KK0  
 ID 068KK0 PRELIMINARY; PRT; 346 AA.

AC 25-OCT-2004 (TREMBLrel. 28, Created)  
 DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)  
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)  
 DE Allergen Sol i 1 precursor.  
 OS Solenopsis invicta (Red imported fire ant).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;  
 OC Formicidae; Myrmicinae; Solenopsis.  
 NCBI\_Taxid=13686;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Venom;  
 RA Schmidt M., Sakell R.H., Hoffman D.R.;  
 RT "The sequence of Sol i 1, the cross-reactive allergen of imported fire ant venom."  
 RL J. Allergy Clin. Immunol. 113:S73-S73(2004).  
 DR EMBL: AY684988; AAT95008.1; -  
 DR InterPro: IPR000734; Lipase.  
 DR InterPro: IPR008262; Lipase\_AS.  
 DR InterPro: IPR000379; Ser esters.  
 DR Pfam: PF00151; Lipase; 1-  
 DR PRINTS: PR00821; TAGLIPASE.  
 DR PROSITE: PS00120; LIPASE\_SER; UNKNOWN\_1.  
 KW SIGNAL.  
 FT CHAIN 1 26 Potential.  
 FT 27 346 Allergen Sol i 1.  
 SQ SEQUENCE 346 AA; 38417 MW; B0A8B8EC6C3DB76BF CRC64;

Query Match 20.5%; Score 353.5; DB 2; Length 346;  
 Best Local Similarity 30.2%; Pred. No. 9.6e-21;  
 Matches 94; Conservative 51; Mismatches 139; Indels 27; Gaps 9;

QY 20 MSPDCPF-NEKDIYFYVSRDKRGILTKKETLNNVLFKSTISKQVFLHGLSTGNG 78  
 DB 36 LKSGCYVGNSSYINVIYHNSR-----FQGNLGNQSCODINASLPEVITTHGFTSSAQ 89  
 QY 79 NENFVANSKALIEKDFLVISVDMKKACNAFASTKDALGYSKAVGNTRHVCKPVAADPTK 138  
 DB 90 VSTFKDLANAFVQGHGTAFI-VDMSAACTDGLPGVQFAEYNAASNTYDIGQLMAKYTV 148

QY 139 LVEKYKVLISNRLIGHSLGHTGSPAGKEVOKLKLGKYEIIIGLDPAQPFYHRSNCPD 198  
 DB 149 DLANCKCIPLNNIQYVHSGSHVCSFAARVKKLTKMPTYLALDPADPSFSSNCKGE 208  
 QY 199 RLCTVDAEYVQVHTSIIIGVYVN-VGSYDFVYVNGKQOPGN--EPCSHTKAVKYLTE 255  
 DB 209 RICKSDPKRIVFRTS-ILSIGENIIGHLIVDPGSGSPACSNVYDPCSHSESVYATG 267  
 QY 256 CIRHECCLIQTPWK-----KYSTPKPISQCRGDTVCVGLNAKSPARGAF 302  
 DB 268 MVSGRCQHLAVPTAQORINPIQKFWRVFTSNIP-AVPTSDFTNCVLTNNVFKNDNTF 326  
 QY 303 YAPYENAPYC 313  
 DB 327 EGEYHA-FPDC 336

## RESULT 13

06PA23  
 ID 06PA23 PRELIMINARY; PRT; 460 AA.

AC 06PA23;  
 DT 05-JUL-2004 (TREMBLrel. 27, Created)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)  
 DE MGC68721 protein.  
 GN Name=MGC68721;  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 NCBI\_Taxid=8355;  
 RX [1]

RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shimen C.M., Schuler G.D.,  
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ueffing T.B., Toshynski S., Carninci P., Prange C.,  
 RA Raha S.S., Loguettano N.A., Peters G.J., Abramson R.D., Mullah S.J.,  
 RA Bosak S.A., McEwan P.C., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,  
 RA Krzywicki M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Cifton S.W.,  
 RA Richardson P.;  
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
 RT Initiative."  
 RL Dev. Dyn. 225:384-391(2002).  
 RN [3]

RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RA Klein S., Strausberg R.,  
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC060482; AA060482.1; -  
 DR GO: GO:0003824; P: catalytic activity; IEA.  
 DR GO: GO:0006229; P: lipid metabolism; IEA.  
 DR InterPro: IPR000734; Lipase.

DR InterPro: IPR008976; Pfam: PF00151; Lipase; 1.  
DR PRINTS: PR00821; TAGLIPASE.  
SQ SEQUENCE 460 AA; 52062 MW; 26502DEA263E3720 CRC64;

Query Match 20.2%; Score 347.5; DB 2; Length 460;  
Best Local Similarity 32.6%; Pred. No. 4.2e-20;  
Matches 93; Conservative 40; Mismatches 105; Indels 47; Gaps 11;

QY 57 FTKSTISKQVFLIHGFLSTGNNENFV-AMSKALIEKDFLIVSVPMKGCANAFSTKD 115  
DB 71 FOYLANTRKTVFLIHGFLSTGNNENFV-AMSKALIEKDFLIVSVPMKGCANAFSTKD 125  
QY 116 ALGYSKAVGNTVRGKVFADFTKLVE---KYKVLISNIRLIGSHSGAHTSPGKGEVOK 172  
DB 126 ---YHNAANTRK---VADILKRLIDNMLSGCATIDSYVMVSVSGAHTSGEVG---K 174  
QY 173 LKLKYEKIIIGLDPAGPYFHRSDCPRLCVTDAEYVQVHTSII-LGVYVNGSVDFPVN 231  
DB 175 MYNGSIGRTIGLDPAGPYFHRSDCPRLCVTDAEYVQVHTSII-LGVYVNGSVDFPVN 234  
QY 232 YGNQPGCNPE-----SCSHTKAVKYLTECIRKHECCIGTPMKKYSTPEKPIQCKG 283  
DB 235 GGTDOGCEPKTIIAGSEYFKCDHQRSVYLYISLKRKCDLVGPCKSY--RDYRIGNCID 292  
QY 284 D-----TCVCVGLNA-----KSPARCAFVAPVEANARYC 313  
DB 293 CKEFLPLSCPVIGFYADKMDHLVEKNPPTKAF--DTAKKDPFC 336

RESULT 14  
Q7OEYS PRELIMINARY; PRT; 576 AA.

AC Q7OEYS; 01-MAR-2004 (TREMBLrel. 26, Created)  
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)  
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
AGCP13285 (Fragment).  
GN Name=agCG47084; ORFNames=ENSNAGS00000010272;  
OS Anopheles gambiae str. PEST.  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.  
OX NCBI\_Taxid=180454;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=PEST.  
RA Anopheles Genome Sequencing Consortium;  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
CC -1- CAUTION: The sequence shown here is derived from an  
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
preliminary data.  
DR EMBL; AAAB01008846; EMBL06347.1; -  
DR HSSP; P54318; 1B08.  
DR GO; GO:0003804; F: catalytic activity; IEA.  
DR GO; GO:0004806; F: triacylglycerol lipase activity; IEA.  
DR GO; GO:0006629; P: lipid metabolism; IEA.  
DR InterPro: IPR000734; Lipase.  
DR InterPro: IPR008262; Lipase\_AS.  
DR InterPro: IPR002331; Lipase\_panc.  
DR InterPro: IPR000379; Ser\_estrs.  
DR Pfam; PF00151; Lipase; 1.  
DR PRINTS; PR00823; PANCCLIPASE.  
DR PRINTS; PR00821; TAGLIPASE.  
DR PROSITE; PS00120; LIPASE\_SER. 1.  
FT NON\_TER 1 1  
SQ SEQUENCE 576 AA; 65067 MW; DBICDF899FF2634F CRC64;

Query Match 20.0%; Score 345; DB 2; Length 576;  
Best Local Similarity 32.0%; Pred. No. 8.7e-20;  
Matches 97; Conservative 42; Mismatches 98; Indels 66; Gaps 12;

QY 65 QVFLIHGFLSTGNNENFVAMSKALIEKDFLIVS---VDMKGCANAFSTKDALGVSK 121

DB 154 RIYFIHTGYIESGDRWRQWIRQNALIENDPDRRTASCVVIDMKR-ASNP-----PYTQ 204  
QY 122 AAGNTRHVKFVADFTKLVEKKYKL-ISNIRLIGSHSGAHTSPGKGEVOK---LKLGR 177  
DB 205 TCANIRLIGATIAHYLYLLYEELNMKNKIDKVLHGLSHGSLCGYAGYHLQKDFKLGR 264  
QY 178 YKEIIGLDPAGPYFHRSDCPRLCVTDAEYVQVHTSII-----LGVYVNGSVDFPVN 230  
DB 265 ---ITGLDPAEPLFSTDTPLVRLDSDAKFVVIHSDGSEWMSKGLMYQPIGHVDFYP 321  
QY 231 NYGNQPGCNPE-----SCSHTKAVKYLTECIRKHECCIGTPMKK 270  
DB 322 NGYVNGSVDFPVN-----SCSHTKAVKYLTECIRKHECCIGTPMKK 381  
QY 271 YESTPEKPIQCKG-----RGPTVCVGLNA-KSP-----ARGAFVAPVEANARY 312  
DB 382 YAQFLR--GECEPCRDGHYCVFGLKQAESYSRLIENGVIKDPNAPLSVMTGAEPY 439  
QY 313 CHN 315  
DB 440 CRS 442

RESULT 15  
Q9VB94 PRELIMINARY; PRT; 676 AA.

AC Q9VB94; 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DE 25-OCT-2004 (TREMBLrel. 28, Last annotation update)  
CG6296-PA (LP07116P).  
GN ORFNames=CG6296;  
OS Drosophila melanogaster (Fruit fly).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
OC Ephydroidea; Drosophilidae; Drosophila.  
OX NCBI\_Taxid=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutten G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.H., Blazef R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,  
RA Abriil J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,  
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borikova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,  
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
RA Flosser C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
RA Harris N.L., Harvey D., Heiman T.T., Hernandez J.R., Houck J.,  
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Idegawa C.,  
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.B., Kethum K.A.,  
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
RA Lascko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
RA Merkulov G., Mikhina N.V., Modyarty C., Morris J., Moshrefi A.,  
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclib J.M.,  
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,  
RA Shue B.C., Sidenkiamos I., Simpson M., Skupski M.P., Smith T.,  
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
RA Svishchak R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissbach J.,



RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,  
 RA Yeh R.F., Zaveri J.S., Zhan W., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426065; PubMed=12537568;  
 RA Celisner S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,  
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,  
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,  
 RA Paclet J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,  
 RA Svirskas R., Taber P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,  
 RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;  
 RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*  
 RT *melanogaster* euchromatic genome sequence.";  
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426070; PubMed=12537573;  
 RA Kaminiker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,  
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,  
 RA Ashburner M., Celisner S.E.;  
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:  
 RT a genomic perspective.";  
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22426069; PubMed=12537572;  
 RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,  
 RA Hradecky P., Huang Y., Kaminiker J.S., Millburn G.H., Pridmore S.E.,  
 RA Smith C.D., Tupy J.L., Whitfield B.J., Bayraktaroglu U., Bertman B.P.,  
 RA Betencourt B.R., Celisner S.E., de Grey A.D., Drysdale R.A.,  
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.O.,  
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,  
 RA Lewis S.E.;  
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a  
 RT systematic review.";  
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RG FlyBase;  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RG FlyBase;  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Berkely;  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,  
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,  
 RA Miranda A., Mungall C.J., Nunoo J., Paclet J., Paragas V., Park S.,  
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
 RA Celisner S.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AEO03758; AAF56648.1; -;  
 DR EMBL; AY118607; AAM49976.1; -;  
 DR HSSP; P54318; 1BU8.  
 DR FlyBase: FBgn0039470; CG6296.  
 DR GO; GO:0003824; F: catalytic activity; IEA.  
 DR GO; GO:0008570; F: phospholipase A1 activity; IEA.  
 DR GO; GO:0006629; P: lipid metabolism; IEA.  
 DR InterPro: IPR002334; DOI/Ves\_allerg.  
 DR InterPro: IPR000734; Lipase.  
 DR InterPro: IPR000379; Ser\_estrs.  
 DR Pfam: PF00151; Lipase\_1.  
 DR PRINTS; PR00825; DOLALBERGEN.  
 DR PRINTS; PR00821; TAGLIPASE.  
 SQ SEQUENCE 676 AA; 72427 MW; 6A707E13C7AC5CCC CRC64;

Query Match 19.9%; Score 342.5; DB 2; Length 676;  
 Best Local Similarity 30.1%; Pred. No. 1.7e-19;  
 Matches 93; Conservative 41; Mismatches 106; Indels 69; Gaps 10;  
 QY 33 FYYV-----SRDKRDGIILKKETLTNYDILFTKSTISKQVFLHGFSLSTGNN 79  
 DB 73 FYLYTLQNPSTGGQIKATQDSIDGSPFNPNR-----ITIHGNSNYKD 118  
 QY 80 ENFVANSKALIEKODFLVLSVDWKKGCACNAFPAKDALGYSKAVGNTRHYGKVADFTKL 139  
 DB 119 GVNTRVADAMFOYGDVYMTAVDMLRG-----SLBYASSVAGAPGAKVAAALYDF 169  
 QY 140 LVKKYKVLINIRLIGHSIGAHNSGFAGKEVQKLKIGKYELIIGLPAGYFHRSDCPDR 199  
 DB 170 LVGGYGLSLDTLTVGSLGAHVAGHTAKVNSGKVGK--VGLDPASPLISYSTEKR 226  
 QY 200 LCVTDAYVYQVINTS-IIIGVYVNVGSVDVYVYVNGKNOGPN--EPCSHTRAVKYLT 255  
 DB 227 LSSDDALVYSIDTNGAILGFGPIGKASFYVNGRSGPCGIDITGSSCHTKAVALYVE 286  
 QY 256 CIRHECCCLIGTPMKKTFSTPKPISQCR-----GDT--CVYGLNAKSPARGAFY 303  
 DB 287 ALP-----WNNF-----PSIKCESSVDANKNNCGNTYSSVFMGASINPFVAEGIFY 332  
 QY 304 APVEANAPY 312  
 DB 333 VPVKNESPY 341

Search completed: April 27, 2005, 12:53:01  
 Job time : 179 secs

**THIS PAGE LEFT BLANK**